

SEQUENCE LISTING

<110> Prayaga, Sudhirdas K.
Majumder, Kumud
Taillon, Bruce E.
Spaderna, Steven K.
Spytek, Kimberly A.
MacDougall, John

<120> NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME

<130> 15966-631

<140> 09/755,665

<141> 2001-01-04

<150> U.S.S.N. 60/174,724

<151> 2000-01-06

<160> 118

<170> PatentIn Ver. 2.1

<210> 1

<211> 559

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (43)..(450)

<400> 1

```

tttctcttct ctgtggacac gcaggcggcc ccggtgactg ag atg gca tcg tct      54
                                     Met Ala Ser Ser
                                     1

cta aag atc tgg ggc aca ctc ttg gcc cta ctt tgc atc cta tgc aca      102
Leu Lys Ile Trp Gly Thr Leu Leu Ala Leu Leu Cys Ile Leu Cys Thr
  5              10              15              20

ctg ctt gta cag agc aaa gaa gtt tct tgg aga gaa ttc atg aaa cag      150
Leu Leu Val Gln Ser Lys Glu Val Ser Trp Arg Glu Phe Met Lys Gln
          25              30              35

cac tac tta agt cca agt cga gaa ttc aga gag tac aaa tgt gat gtc      198
His Tyr Leu Ser Pro Ser Arg Glu Phe Arg Glu Tyr Lys Cys Asp Val
          40              45              50

ctc atg aga gaa aat gaa gct ctg aaa gac aag agc tct cac atg ttt      246
Leu Met Arg Glu Asn Glu Ala Leu Lys Asp Lys Ser Ser His Met Phe
          55              60              65

atc tat atc tca tgg tac aaa atc gag cat ata tgc act agt gac aac      294
Ile Tyr Ile Ser Trp Tyr Lys Ile Glu His Ile Cys Thr Ser Asp Asn
          70              75              80

```

tgg atg gat cgc ttc cga aat gca tat gta tgg gtc cag atc ctc tca 342
 Trp Met Asp Arg Phe Arg Asn Ala Tyr Val Trp Val Gln Ile Leu Ser
 85 90 95 100

 aag tac tca agt gtc acc agg aga att cca aaa ata gct aca cag aga 390
 Lys Tyr Ser Ser Val Thr Arg Arg Ile Pro Lys Ile Ala Thr Gln Arg
 105 110 115

 gca gga gct tca act aca ttg aat tcc att gta gca tgg acg ggt atg 438
 Ala Gly Ala Ser Thr Thr Leu Asn Ser Ile Val Ala Trp Thr Gly Met
 120 125 130

 ttg ata gca tag aagacctaaa gatggtagaa cctatcggca actagaaagt 490
 Leu Ile Ala
 135

 cstatgcacat cctcaggtat tggtagagta ttcagtgctt tctaagtagc agccccctgcc 550
 tccatcaat 559

<210> 2
 <211> 135
 <212> PRT
 <213> Homo sapiens

<400> 2
 Met Ala Ser Ser Leu Lys Ile Trp Gly Thr Leu Leu Ala Leu Leu Cys
 1 5 10 15
 Ile Leu Cys Thr Leu Leu Val Gln Ser Lys Glu Val Ser Trp Arg Glu
 20 25 30
 Phe Met Lys Gln His Tyr Leu Ser Pro Ser Arg Glu Phe Arg Glu Tyr
 35 40 45
 Lys Cys Asp Val Leu Met Arg Glu Asn Glu Ala Leu Lys Asp Lys Ser
 50 55 60
 Ser His Met Phe Ile Tyr Ile Ser Trp Tyr Lys Ile Glu His Ile Cys
 65 70 75 80
 Thr Ser Asp Asn Trp Met Asp Arg Phe Arg Asn Ala Tyr Val Trp Val
 85 90 95
 Gln Ile Leu Ser Lys Tyr Ser Ser Val Thr Arg Arg Ile Pro Lys Ile
 100 105 110
 Ala Thr Gln Arg Ala Gly Ala Ser Thr Thr Leu Asn Ser Ile Val Ala
 115 120 125
 Trp Thr Gly Met Leu Ile Ala
 130 135

<210> 3
 <211> 425
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (16)..(417)

<400> 3

```

gccccggtga ctgag atg gca tcc tct ctg aag atc tgg ggc agt ccc ttg 51
      Met Ala Ser Ser Leu Lys Ile Trp Gly Ser Pro Leu
            1                    5                    10

gcc ctg ctt tgc att ctt tgc agg cta ctt gta cac agc aag gac gtt 99
Ala Leu Leu Cys Ile Leu Cys Arg Leu Leu Val His Ser Lys Asp Val
            15                    20                    25

tcc tgg aga gaa ttc atg acc ctg cac tat tta gat cca agc caa gat 147
Ser Trp Arg Glu Phe Met Thr Leu His Tyr Leu Asp Pro Ser Gln Asp
            30                    35                    40

ttt gaa gag tac aaa tgt gat gtc ctc atg aga gaa aaa gaa gct ctg 195
Phe Glu Glu Tyr Lys Cys Asp Val Leu Met Arg Glu Lys Glu Ala Leu
            45                    50                    55                    60

aaa cgc aag agc tct cat atg tcc atc tat agc tta tgg cac aaa atg 243
Lys Arg Lys Ser Ser His Met Ser Ile Tyr Ser Leu Trp His Lys Met
            65                    70                    75

gag tgt ata tgc att att gaa atg gga ata acc gat ata gat atg cct 291
Glu Cys Ile Cys Ile Ile Glu Met Gly Ile Thr Asp Ile Asp Met Pro
            80                    85                    90

atg tat ggg ccc agg gtg ccc tca aag tac tgc agt gtc agt ggc aga 339
Met Tyr Gly Pro Arg Val Pro Ser Lys Tyr Ser Ser Val Ser Gly Arg
            95                    100                    105

agt act gca ata gct aca cag aga tct tca act aca ttg aat tcc act 387
Ser Thr Ala Ile Ala Thr Gln Arg Ser Ser Thr Thr Leu Asn Ser Thr
            110                    115                    120

gtg gca agg atg ggt atg ttg ata gca tag aagaccta 425
Val Ala Arg Met Gly Met Leu Ile Ala
125                    130

```

<210> 4

<211> 133

<212> PRT

<213> Homo sapiens

<400> 4

```

Met Ala Ser Ser Leu Lys Ile Trp Gly Ser Pro Leu Ala Leu Leu Cys
  1                    5                    10                    15
Ile Leu Cys Arg Leu Leu Val His Ser Lys Asp Val Ser Trp Arg Glu
            20                    25                    30
Phe Met Thr Leu His Tyr Leu Asp Pro Ser Gln Asp Phe Glu Glu Tyr
            35                    40                    45
Lys Cys Asp Val Leu Met Arg Glu Lys Glu Ala Leu Lys Arg Lys Ser
            50                    55                    60
Ser His Met Ser Ile Tyr Ser Leu Trp His Lys Met Glu Cys Ile Cys
            65                    70                    75                    80
Ile Ile Glu Met Gly Ile Thr Asp Ile Asp Met Pro Met Tyr Gly Pro
            85                    90                    95
Arg Val Pro Ser Lys Tyr Ser Ser Val Ser Gly Arg Ser Thr Ala Ile

```

	100		105		110
Ala Thr Gln Arg Ser Ser Thr Thr Leu Asn Ser Thr Val Ala Arg Met					
	115		120		125
Gly Met Leu Ile Ala					
130					

<210> 5
 <211> 554
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (44)..(487)

<400> 5	
ttttctcttc tctgtggaca cgcaggcggc cccggtgact gag atg gca tca tct	55
	Met Ala Ser Ser
	1
cta aag atc tgg ggc aca ctc ttg gcc cta ctt tgc atc cta tgc aca	103
Leu Lys Ile Trp Gly Thr Leu Leu Ala Leu Leu Cys Ile Leu Cys Thr	
5 10 15 20	
ctg ctt gta cag agc aaa gaa gtt tct tgg aga gaa ttc atg aaa cag	151
Leu Leu Val Gln Ser Lys Glu Val Ser Trp Arg Glu Phe Met Lys Gln	
25 30 35	
cac tac tta agt cca agt cga gaa ttc aga gag tac aaa tgt gat gtc	199
His Tyr Leu Ser Pro Ser Arg Glu Phe Arg Glu Tyr Lys Cys Asp Val	
40 45 50	
ctc atg aga gaa aat gaa gct ctg aaa gac aag agc tct cac atg ttt	247
Leu Met Arg Glu Asn Glu Ala Leu Lys Asp Lys Ser Ser His Met Phe	
55 60 65	
atc tat atc tca tgg tac aaa atc gag cat ata tgc act agt gac aac	295
Ile Tyr Ile Ser Trp Tyr Lys Ile Glu His Ile Cys Thr Ser Asp Asn	
70 75 80	
tgg atg gat cgc ttc cga aat gca tat gta tgg gtc cag aat cct ctc	343
Trp Met Asp Arg Phe Arg Asn Ala Tyr Val Trp Val Gln Asn Pro Leu	
85 90 95 100	
aaa gta ctc aag tgt cac cag gag aat tcc aaa aat agc tac aca gag	391
Lys Val Leu Lys Cys His Gln Glu Asn Ser Lys Asn Ser Tyr Thr Glu	
105 110 115	
agc agg agc ttc aac tac att gaa ttc cat tgt agc atg gac ggg tat	439
Ser Arg Ser Phe Asn Tyr Ile Glu Phe His Cys Ser Met Asp Gly Tyr	
120 125 130	
gtt gat agc ata gaa gac cta aag atg gta gaa cct atc ggc aac tag	487
Val Asp Ser Ile Glu Asp Leu Lys Met Val Glu Pro Ile Gly Asn	
135 140 145	

aaagtctatg cacatcctca ggtattggta gagtattcag tgctttctaa gtagcagccc 547

aagggcg 554

<210> 6
 <211> 147
 <212> PRT
 <213> Homo sapiens

<400> 6
 Met Ala Ser Ser Leu Lys Ile Trp Gly Thr Leu Leu Ala Leu Leu Cys
 1 5 10 15
 Ile Leu Cys Thr Leu Leu Val Gln Ser Lys Glu Val Ser Trp Arg Glu
 20 25 30
 Phe Met Lys Gln His Tyr Leu Ser Pro Ser Arg Glu Phe Arg Glu Tyr
 35 40 45
 Lys Cys Asp Val Leu Met Arg Glu Asn Glu Ala Leu Lys Asp Lys Ser
 50 55 60
 Ser His Met Phe Ile Tyr Ile Ser Trp Tyr Lys Ile Glu His Ile Cys
 65 70 75 80
 Thr Ser Asp Asn Trp Met Asp Arg Phe Arg Asn Ala Tyr Val Trp Val
 85 90 95
 Gln Asn Pro Leu Lys Val Leu Lys Cys His Gln Glu Asn Ser Lys Asn
 100 105 110
 Ser Tyr Thr Glu Ser Arg Ser Phe Asn Tyr Ile Glu Phe His Cys Ser
 115 120 125
 Met Asp Gly Tyr Val Asp Ser Ile Glu Asp Leu Lys Met Val Glu Pro
 130 135 140
 Ile Gly Asn
 145

<210> 7
 <211> 1300
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (59)..(1201)

<220>
 <221> misc_feature
 <222> (1218)
 <223> Wherein n is G or A or T or C

<400> 7
 gcccgccac tacgggccca ggctagaggc gccgcccga ccggcccgcg gagcccg 58

atg ctg gcc cgg agg aag ccg atg ctg ccg gcg ctc acc atc aac cct 106
 Met Leu Ala Arg Arg Lys Pro Met Leu Pro Ala Leu Thr Ile Asn Pro
 1 5 10 15

acc atc gcc gag ggc ccg tcc cca acc agc gag ggc gcc tcc gag gca 154

Thr	Ile	Ala	Glu	Gly	Pro	Ser	Pro	Thr	Ser	Glu	Gly	Ala	Ser	Glu	Ala		
			20					25					30				
aac	ctg	gtg	gac	ctg	cag	aag	aag	ctg	gag	gag	ctg	gaa	ctt	gac	gag	202	
Asn	Leu	Val	Asp	Leu	Gln	Lys	Lys	Leu	Glu	Glu	Leu	Glu	Leu	Asp	Glu		
		35					40					45					
cag	cag	aag	cgg	ctg	gaa	gcc	ttt	ctc	acc	cag	aaa	gcc	aag	gtc	ggc	250	
Gln	Gln	Lys	Arg	Leu	Glu	Ala	Phe	Leu	Thr	Gln	Lys	Ala	Lys	Val	Gly		
		50				55					60						
gaa	ctc	aaa	gac	gat	gac	ttc	gaa	agg	acc	tca	gag	ctg	gac	gcg	ggc	298	
Glu	Leu	Lys	Asp	Asp	Asp	Phe	Glu	Arg	Thr	Ser	Glu	Leu	Asp	Ala	Gly		
	65				70				75						80		
aac	ggc	ggg	gtg	gtc	acc	aaa	gtc	cag	cac	aga	ccc	tcg	ggc	ctc	atc	346	
Asn	Gly	Gly	Val	Val	Thr	Lys	Val	Gln	His	Arg	Pro	Ser	Gly	Leu	Ile		
				85					90					95			
atg	gcc	agg	aag	ctg	atc	cac	ctt	gag	atc	aag	ccg	gcc	atc	cgg	aac	394	
Met	Ala	Arg	Lys	Leu	Ile	His	Leu	Glu	Ile	Lys	Pro	Ala	Ile	Arg	Asn		
			100					105					110				
cag	atc	atc	cgc	gag	cac	cag	gtc	ctg	cac	gag	tgc	aac	tca	ccg	tac	442	
Gln	Ile	Ile	Arg	Glu	His	Gln	Val	Leu	His	Glu	Cys	Asn	Ser	Pro	Tyr		
			115				120					125					
atc	gtg	ggc	ttc	tac	ggg	gcc	ttc	tac	tgt	gac	agg	gag	atc	agc	atc	490	
Ile	Val	Gly	Phe	Tyr	Gly	Ala	Phe	Tyr	Cys	Asp	Arg	Glu	Ile	Ser	Ile		
	130					135					140						
tgc	atg	gag	cac	atg	gat	ggc	ggc	tcc	ctg	gac	cag	ggg	ctg	aaa	gag	538	
Cys	Met	Glu	His	Met	Asp	Gly	Gly	Ser	Leu	Asp	Gln	Gly	Leu	Lys	Glu		
	145				150					155					160		
gcc	aag	agg	att	ccc	gag	gac	atc	ctg	ggg	aaa	gtc	agc	att	gcg	gtt	586	
Ala	Lys	Arg	Ile	Pro	Glu	Asp	Ile	Leu	Gly	Lys	Val	Ser	Ile	Ala	Val		
				165					170					175			
ctc	cgg	ggc	ttg	gcg	tac	ctc	cga	gag	aag	cac	cag	atc	atg	cac	cga	634	
Leu	Arg	Gly	Leu	Ala	Tyr	Leu	Arg	Glu	Lys	His	Gln	Ile	Met	His	Arg		
			180					185					190				
aat	gtg	aag	ccc	tcc	aac	atc	ctc	gtg	aac	tct	aga	ggg	gag	atc	aag	682	
Asn	Val	Lys	Pro	Ser	Asn	Ile	Leu	Val	Asn	Ser	Arg	Gly	Glu	Ile	Lys		
		195					200					205					
ctg	tgt	gac	ttc	ggg	gtg	agc	ggc	cag	ctc	atc	gac	tcc	atg	gcc	aac	730	
Leu	Cys	Asp	Phe	Gly	Val	Ser	Gly	Gln	Leu	Ile	Asp	Ser	Met	Ala	Asn		
	210					215					220						
tcc	ttc	gtg	ggc	acg	cgc	tcc	tac	atg	gct	ccg	gag	cgg	ttg	cag	ggc	778	
Ser	Phe	Val	Gly	Thr	Arg	Ser	Tyr	Met	Ala	Pro	Glu	Arg	Leu	Gln	Gly		
	225				230					235					240		
aca	cat	tac	tcg	gtg	cag	tcg	gtc	atc	tgg	agc	atg	gac	ctg	tcc	ctg	826	
Thr	His	Tyr	Ser	Val	Gln	Ser	Val	Ile	Trp	Ser	Met	Asp	Leu	Ser	Leu		

245	250	255	
gtg gag ctg gcc atc gaa agg tac ccc atc ccc ccg ccc gac gcc aag			874
Val Glu Leu Ala Ile Glu Arg Tyr Pro Ile Pro Pro Pro Asp Ala Lys			
260	265	270	
gag ctg gag gcc atc ttt ggc cag ccc gtg gtc gac agg gaa gaa gga			922
Glu Leu Glu Ala Ile Phe Gly Gln Pro Val Val Asp Arg Glu Glu Gly			
275	280	285	
gag cct cac agc atc tcc tct tgg cca ggg tcc ccc ggg cgc ccc aac			970
Glu Pro His Ser Ile Ser Ser Trp Pro Gly Ser Pro Gly Arg Pro Asn			
290	295	300	
agc ggt tac ggg atg gac agc ctg ccc gcc atg gcc atc ttc gaa ctg			1018
Ser Gly Tyr Gly Met Asp Ser Leu Pro Ala Met Ala Ile Phe Glu Leu			
305	310	315	320
ctg gac tat att gtg aaa gag ccg cct cct aag ctg ccc aac ggt gtg			1066
Leu Asp Tyr Ile Val Lys Glu Pro Pro Pro Lys Leu Pro Asn Gly Val			
325	330	335	
ttc acc ccc gag ttc cag gag ttt gtc aat aaa tgc ctc atc aaa aac			1114
Phe Thr Pro Glu Phe Gln Glu Phe Val Asn Lys Cys Leu Ile Lys Asn			
340	345	350	
cca acg gag cgg gcg gac cta aag atg ctc aca aac cac gcc ttc atc			1162
Pro Thr Glu Arg Ala Asp Leu Lys Met Leu Thr Asn His Ala Phe Ile			
355	360	365	
aag cgg tcc gag gtg aaa gaa gcg gat ttt gcc tgc tag ttgtgtaaaa			1211
Lys Arg Ser Glu Val Lys Glu Ala Asp Phe Ala Cys			
370	375	380	
ccctggnngc tgaaccaagc ccggcacacc cacgcgcacc gccgtgtaca gtggcaggct			1271
ccccgcgtcc gctggtgact gcccacgca			1300

<210> 8

<211> 380

<212> PRT

<213> Homo sapiens

<400> 8

Met	Leu	Ala	Arg	Arg	Lys	Pro	Met	Leu	Pro	Ala	Leu	Thr	Ile	Asn	Pro
1				5					10					15	
Thr	Ile	Ala	Glu	Gly	Pro	Ser	Pro	Thr	Ser	Glu	Gly	Ala	Ser	Glu	Ala
		20						25					30		
Asn	Leu	Val	Asp	Leu	Gln	Lys	Lys	Leu	Glu	Glu	Leu	Glu	Leu	Asp	Glu
		35				40					45				
Gln	Gln	Lys	Arg	Leu	Glu	Ala	Phe	Leu	Thr	Gln	Lys	Ala	Lys	Val	Gly
	50					55				60					
Glu	Leu	Lys	Asp	Asp	Asp	Phe	Glu	Arg	Thr	Ser	Glu	Leu	Asp	Ala	Gly
	65				70				75					80	
Asn	Gly	Gly	Val	Val	Thr	Lys	Val	Gln	His	Arg	Pro	Ser	Gly	Leu	Ile
			85					90						95	

Met	Ala	Arg	Lys	Leu	Ile	His	Leu	Glu	Ile	Lys	Pro	Ala	Ile	Arg	Asn
			100					105					110		
Gln	Ile	Ile	Arg	Glu	His	Gln	Val	Leu	His	Glu	Cys	Asn	Ser	Pro	Tyr
		115					120					125			
Ile	Val	Gly	Phe	Tyr	Gly	Ala	Phe	Tyr	Cys	Asp	Arg	Glu	Ile	Ser	Ile
		130				135					140				
Cys	Met	Glu	His	Met	Asp	Gly	Gly	Ser	Leu	Asp	Gln	Gly	Leu	Lys	Glu
145					150					155					160
Ala	Lys	Arg	Ile	Pro	Glu	Asp	Ile	Leu	Gly	Lys	Val	Ser	Ile	Ala	Val
			165						170					175	
Leu	Arg	Gly	Leu	Ala	Tyr	Leu	Arg	Glu	Lys	His	Gln	Ile	Met	His	Arg
		180						185					190		
Asn	Val	Lys	Pro	Ser	Asn	Ile	Leu	Val	Asn	Ser	Arg	Gly	Glu	Ile	Lys
		195					200					205			
Leu	Cys	Asp	Phe	Gly	Val	Ser	Gly	Gln	Leu	Ile	Asp	Ser	Met	Ala	Asn
	210					215					220				
Ser	Phe	Val	Gly	Thr	Arg	Ser	Tyr	Met	Ala	Pro	Glu	Arg	Leu	Gln	Gly
225					230				235						240
Thr	His	Tyr	Ser	Val	Gln	Ser	Val	Ile	Trp	Ser	Met	Asp	Leu	Ser	Leu
			245					250					255		
Val	Glu	Leu	Ala	Ile	Glu	Arg	Tyr	Pro	Ile	Pro	Pro	Pro	Asp	Ala	Lys
			260					265					270		
Glu	Leu	Glu	Ala	Ile	Phe	Gly	Gln	Pro	Val	Val	Asp	Arg	Glu	Glu	Gly
	275					280					285				
Glu	Pro	His	Ser	Ile	Ser	Ser	Trp	Pro	Gly	Ser	Pro	Gly	Arg	Pro	Asn
	290				295						300				
Ser	Gly	Tyr	Gly	Met	Asp	Ser	Leu	Pro	Ala	Met	Ala	Ile	Phe	Glu	Leu
305					310				315						320
Leu	Asp	Tyr	Ile	Val	Lys	Glu	Pro	Pro	Pro	Lys	Leu	Pro	Asn	Gly	Val
			325					330					335		
Phe	Thr	Pro	Glu	Phe	Gln	Glu	Phe	Val	Asn	Lys	Cys	Leu	Ile	Lys	Asn
			340					345					350		
Pro	Thr	Glu	Arg	Ala	Asp	Leu	Lys	Met	Leu	Thr	Asn	His	Ala	Phe	Ile
		355				360					365				
Lys	Arg	Ser	Glu	Val	Lys	Glu	Ala	Asp	Phe	Ala	Cys				
	370					375					380				

<210> 9
 <211> 324
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(324)

<400> 9																
atg	cca	ccc	tgc	agc	tgt	gcc	aga	tca	ctt	tgt	gcc	ctg	cag	gtg	ctg	48
Met	Pro	Pro	Cys	Ser	Cys	Ala	Arg	Ser	Leu	Cys	Ala	Leu	Gln	Val	Leu	
1				5					10					15		
ctg ttg act gtt ctg ggt tcc tcc acc aat gga caa act aag aga aac																96
Leu	Leu	Thr	Val	Leu	Gly	Ser	Ser	Thr	Asn	Gly	Gln	Thr	Lys	Arg	Asn	
			20					25					30			

ata ggg aaa agt gta gac agt gac ttg tac act gaa ctg cgc tgc gtg 144
 Ile Gly Lys Ser Val Asp Ser Asp Leu Tyr Thr Glu Leu Arg Cys Val
 35 40 45

 tat gtg aag tca acc ttt gta ctt cat ccc aga aac atc cac aat ttg 192
 Tyr Val Lys Ser Thr Phe Val Leu His Pro Arg Asn Ile His Asn Leu
 50 55 60

 gag ttg gtc tca gca gga ccc cat tgc agc aaa gac gaa gaa aaa atc 240
 Glu Leu Val Ser Ala Gly Pro His Cys Ser Lys Asp Glu Glu Lys Ile
 65 70 75 80

 tgc ctg gac cca gat gct ccc aga atc aat aaa att gta cag aaa atg 288
 Cys Leu Asp Pro Asp Ala Pro Arg Ile Asn Lys Ile Val Gln Lys Met
 85 90 95

 ttg aaa gtt gat gaa ttc atc tgg tta att tgt taa 324
 Leu Lys Val Asp Glu Phe Ile Trp Leu Ile Cys
 100 105

<210> 10
 <211> 107
 <212> PRT
 <213> Homo sapiens

<400> 10
 Met Pro Pro Cys Ser Cys Ala Arg Ser Leu Cys Ala Leu Gln Val Leu
 1 5 10 15
 Leu Leu Thr Val Leu Gly Ser Ser Thr Asn Gly Gln Thr Lys Arg Asn
 20 25 30
 Ile Gly Lys Ser Val Asp Ser Asp Leu Tyr Thr Glu Leu Arg Cys Val
 35 40 45
 Tyr Val Lys Ser Thr Phe Val Leu His Pro Arg Asn Ile His Asn Leu
 50 55 60
 Glu Leu Val Ser Ala Gly Pro His Cys Ser Lys Asp Glu Glu Lys Ile
 65 70 75 80
 Cys Leu Asp Pro Asp Ala Pro Arg Ile Asn Lys Ile Val Gln Lys Met
 85 90 95
 Leu Lys Val Asp Glu Phe Ile Trp Leu Ile Cys
 100 105

<210> 11
 <211> 300
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(300)

<400> 11
 atg act tct aag ctg gct gtt gct cta ctg ctt ctt ggc agt tgc atg 48
 Met Thr Ser Lys Leu Ala Val Ala Leu Leu Leu Leu Gly Ser Cys Met
 1 5 10 15

ctt tct gta gca ctg tgt gaa gtg cca agt att agt aca gta cca caa	96
Leu Ser Val Ala Leu Cys Glu Val Pro Ser Ile Ser Thr Val Pro Gln	
20 25 30	
tgc cag tgc atg agg aca cat ttt ata cct ttg cat ccc aaa ttt att	144
Cys Gln Cys Met Arg Thr His Phe Ile Pro Leu His Pro Lys Phe Ile	
35 40 45	
aaa gaa ctc aga att att cag gta ctt tca aaa gtt ctt agt tat ttt	192
Lys Glu Leu Arg Ile Ile Gln Val Leu Ser Lys Val Leu Ser Tyr Phe	
50 55 60	
gct tct gta cat gta gac tgt tta ggt gct gag agt aca atg gta aac	240
Ala Ser Val His Val Asp Cys Leu Gly Ala Glu Ser Thr Met Val Asn	
65 70 75 80	
aga aca gca aaa aaa aaa aat tct gtc ttt aca aat aac ttg gta ctg	288
Arg Thr Ala Lys Lys Lys Asn Ser Val Phe Thr Asn Asn Leu Val Leu	
85 90 95	
aca tct ggt tag	300
Thr Ser Gly	
100	

<210> 12
 <211> 99
 <212> PRT
 <213> Homo sapiens

<400> 12
Met Thr Ser Lys Leu Ala Val Ala Leu Leu Leu Leu Gly Ser Cys Met
1 5 10 15
Leu Ser Val Ala Leu Cys Glu Val Pro Ser Ile Ser Thr Val Pro Gln
20 25 30
Cys Gln Cys Met Arg Thr His Phe Ile Pro Leu His Pro Lys Phe Ile
35 40 45
Lys Glu Leu Arg Ile Ile Gln Val Leu Ser Lys Val Leu Ser Tyr Phe
50 55 60
Ala Ser Val His Val Asp Cys Leu Gly Ala Glu Ser Thr Met Val Asn
65 70 75 80
Arg Thr Ala Lys Lys Asn Ser Val Phe Thr Asn Asn Leu Val Leu
85 90 95
Thr Ser Gly

<210> 13
 <211> 1245
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(1245)

<400> 13

atg aac ccc aca cta ggc ctg gcc att ttt ctg gct gtt ctc ctc acg	48
Met Asn Pro Thr Leu Gly Leu Ala Ile Phe Leu Ala Val Leu Leu Thr	
1 5 10 15	
gtg aaa ggt ctt cta aag ccg agc ttc tca cca agg aat tat aaa gct	96
Val Lys Gly Leu Leu Lys Pro Ser Phe Ser Pro Arg Asn Tyr Lys Ala	
20 25 30	
ttg agc gag gtc caa gga tgg aag caa agg atg gca gcc aag gag ctt	144
Leu Ser Glu Val Gln Gly Trp Lys Gln Arg Met Ala Ala Lys Glu Leu	
35 40 45	
gca agg cag aac atg gac tta ggc ttt aag ctg ctc aag aag ctg gcc	192
Ala Arg Gln Asn Met Asp Leu Gly Phe Lys Leu Leu Lys Lys Leu Ala	
50 55 60	
ttt tac aac cct ggc agg aac atc ttc cta tcc ccc ttg agc atc tct	240
Phe Tyr Asn Pro Gly Arg Asn Ile Phe Leu Ser Pro Leu Ser Ile Ser	
65 70 75 80	
aca gct ttc tcc atg ctg tgc ctg ggt gcc cag gac agc acc ctg gac	288
Thr Ala Phe Ser Met Leu Cys Leu Gly Ala Gln Asp Ser Thr Leu Asp	
85 90 95	
gag atc aag cag ggg ttc aac ttc aga aag atg cca gaa aaa gat ctt	336
Glu Ile Lys Gln Gly Phe Asn Phe Arg Lys Met Pro Glu Lys Asp Leu	
100 105 110	
cat gag ggc ttc cat tac atc atc cac gag ctg acc cag aag acc cag	384
His Glu Gly Phe His Tyr Ile Ile His Glu Leu Thr Gln Lys Thr Gln	
115 120 125	
gac ctc aaa ctg agc att ggg aac acg ctg ttc att gac cag agg ctg	432
Asp Leu Lys Leu Ser Ile Gly Asn Thr Leu Phe Ile Asp Gln Arg Leu	
130 135 140	
cag cca cag cgt aag ttt ttg gaa gat gcc aag aac ttt tac agt gcc	480
Gln Pro Gln Arg Lys Phe Leu Glu Asp Ala Lys Asn Phe Tyr Ser Ala	
145 150 155 160	
gaa acc atc ctt acc aac ttt cag aat ttg gaa atg gct cag aag cag	528
Glu Thr Ile Leu Thr Asn Phe Gln Asn Leu Glu Met Ala Gln Lys Gln	
165 170 175	
atc aat gac ttt atc agt caa aaa acc cat ggg aaa att aac aac ctg	576
Ile Asn Asp Phe Ile Ser Gln Lys Thr His Gly Lys Ile Asn Asn Leu	
180 185 190	
atc gag aat ata gac ccc ggc act gtg atg ctt ctt gca aat tat att	624
Ile Glu Asn Ile Asp Pro Gly Thr Val Met Leu Leu Ala Asn Tyr Ile	
195 200 205	
ttc ttt cga gcc agg tgg aaa cat gag ttt gat cca aat gta act aaa	672
Phe Phe Arg Ala Arg Trp Lys His Glu Phe Asp Pro Asn Val Thr Lys	
210 215 220	

gag gaa gat ttc ttt ctg gag aaa aac agt tca gtc aag gtg ccc atg	720
Glu Glu Asp Phe Phe Leu Glu Lys Asn Ser Ser Val Lys Val Pro Met	
225 230 235 240	
atg ttc cgt agt ggc ata tac caa gtt ggc tat gac gat aag ctc tct	768
Met Phe Arg Ser Gly Ile Tyr Gln Val Gly Tyr Asp Asp Lys Leu Ser	
245 250 255	
tgc acc atc ctg gaa ata ccc tac cag aaa aat atc aca gcc atc ttc	816
Cys Thr Ile Leu Glu Ile Pro Tyr Gln Lys Asn Ile Thr Ala Ile Phe	
260 265 270	
atc ctt cct gat gag ggc aag ctg aag cac ttg gag aag gga ttg cag	864
Ile Leu Pro Asp Glu Gly Lys Leu Lys His Leu Glu Lys Gly Leu Gln	
275 280 285	
gtg gac act ttc tcc aga tgg aaa aca tta ctg tca cgc agg gtc gta	912
Val Asp Thr Phe Ser Arg Trp Lys Thr Leu Leu Ser Arg Arg Val Val	
290 295 300	
gac gtg tct gta ccc aga ctc cac atg acg ggc acc ttc gac ctg aag	960
Asp Val Ser Val Pro Arg Leu His Met Thr Gly Thr Phe Asp Leu Lys	
305 310 315 320	
aag act ctc tcc tac ata ggt gtc tcc aaa atc ttt gag gaa cat ggt	1008
Lys Thr Leu Ser Tyr Ile Gly Val Ser Lys Ile Phe Glu Glu His Gly	
325 330 335	
gat ctc acc aag atc gcc cct cat cgc agc ctg aaa gtg ggc gag gct	1056
Asp Leu Thr Lys Ile Ala Pro His Arg Ser Leu Lys Val Gly Glu Ala	
340 345 350	
gtg cac aag gct gag ctg aag atg gat gag agg ggt acg gaa ggg gcc	1104
Val His Lys Ala Glu Leu Lys Met Asp Glu Arg Gly Thr Glu Gly Ala	
355 360 365	
gct ggc acc gga gca cag act ctg ccc atg gag aca cca ctc gtc gtc	1152
Ala Gly Thr Gly Ala Gln Thr Leu Pro Met Glu Thr Pro Leu Val Val	
370 375 380	
aag ata gac aaa ccc tat ctg ctg ctg att tac agc gag aaa ata cct	1200
Lys Ile Asp Lys Pro Tyr Leu Leu Leu Ile Tyr Ser Glu Lys Ile Pro	
385 390 395 400	
tcc gtg ctc ttc ctg gga aag att gtt aac cct att gga aaa taa	1245
Ser Val Leu Phe Leu Gly Lys Ile Val Asn Pro Ile Gly Lys	
405 410 415	

<210> 14

<211> 414

<212> PRT

<213> Homo sapiens

<400> 14

Met Asn Pro Thr Leu Gly Leu Ala Ile Phe Leu Ala Val Leu Leu Thr
1 5 10 15

Val	Lys	Gly	Leu	Leu	Lys	Pro	Ser	Phe	Ser	Pro	Arg	Asn	Tyr	Lys	Ala		
			20					25					30				
Leu	Ser	Glu	Val	Gln	Gly	Trp	Lys	Gln	Arg	Met	Ala	Ala	Lys	Glu	Leu		
		35					40					45					
Ala	Arg	Gln	Asn	Met	Asp	Leu	Gly	Phe	Lys	Leu	Leu	Lys	Lys	Leu	Ala		
	50					55					60						
Phe	Tyr	Asn	Pro	Gly	Arg	Asn	Ile	Phe	Leu	Ser	Pro	Leu	Ser	Ile	Ser		
	65				70					75				80			
Thr	Ala	Phe	Ser	Met	Leu	Cys	Leu	Gly	Ala	Gln	Asp	Ser	Thr	Leu	Asp		
			85					90						95			
Glu	Ile	Lys	Gln	Gly	Phe	Asn	Phe	Arg	Lys	Met	Pro	Glu	Lys	Asp	Leu		
		100						105					110				
His	Glu	Gly	Phe	His	Tyr	Ile	Ile	His	Glu	Leu	Thr	Gln	Lys	Thr	Gln		
		115				120						125					
Asp	Leu	Lys	Leu	Ser	Ile	Gly	Asn	Thr	Leu	Phe	Ile	Asp	Gln	Arg	Leu		
	130					135					140						
Gln	Pro	Gln	Arg	Lys	Phe	Leu	Glu	Asp	Ala	Lys	Asn	Phe	Tyr	Ser	Ala		
	145				150					155					160		
Glu	Thr	Ile	Leu	Thr	Asn	Phe	Gln	Asn	Leu	Glu	Met	Ala	Gln	Lys	Gln		
			165					170						175			
Ile	Asn	Asp	Phe	Ile	Ser	Gln	Lys	Thr	His	Gly	Lys	Ile	Asn	Asn	Leu		
		180						185					190				
Ile	Glu	Asn	Ile	Asp	Pro	Gly	Thr	Val	Met	Leu	Leu	Ala	Asn	Tyr	Ile		
	195					200						205					
Phe	Phe	Arg	Ala	Arg	Trp	Lys	His	Glu	Phe	Asp	Pro	Asn	Val	Thr	Lys		
	210				215					220							
Glu	Glu	Asp	Phe	Phe	Leu	Glu	Lys	Asn	Ser	Ser	Val	Lys	Val	Pro	Met		
				230					235						240		
Met	Phe	Arg	Ser	Gly	Ile	Tyr	Gln	Val	Gly	Tyr	Asp	Asp	Lys	Leu	Ser		
			245						250					255			
Cys	Thr	Ile	Leu	Glu	Ile	Pro	Tyr	Gln	Lys	Asn	Ile	Thr	Ala	Ile	Phe		
		260						265					270				
Ile	Leu	Pro	Asp	Glu	Gly	Lys	Leu	Lys	His	Leu	Glu	Lys	Gly	Leu	Gln		
		275					280					285					
Val	Asp	Thr	Phe	Ser	Arg	Trp	Lys	Thr	Leu	Leu	Ser	Arg	Arg	Val	Val		
	290					295					300						
Asp	Val	Ser	Val	Pro	Arg	Leu	His	Met	Thr	Gly	Thr	Phe	Asp	Leu	Lys		
	305				310					315				320			
Lys	Thr	Leu	Ser	Tyr	Ile	Gly	Val	Ser	Lys	Ile	Phe	Glu	Glu	His	Gly		
			325						330					335			
Asp	Leu	Thr	Lys	Ile	Ala	Pro	His	Arg	Ser	Leu	Lys	Val	Gly	Glu	Ala		
		340						345					350				
Val	His	Lys	Ala	Glu	Leu	Lys	Met	Asp	Glu	Arg	Gly	Thr	Glu	Gly	Ala		
		355					360					365					
Ala	Gly	Thr	Gly	Ala	Gln	Thr	Leu	Pro	Met	Glu	Thr	Pro	Leu	Val	Val		
	370					375					380						
Lys	Ile	Asp	Lys	Pro	Tyr	Leu	Leu	Leu	Ile	Tyr	Ser	Glu	Lys	Ile	Pro		
	385				390					395					400		
Ser	Val	Leu	Phe	Leu	Gly	Lys	Ile	Val	Asn	Pro	Ile	Gly	Lys				
			405					410									

<210> 15

<211> 1123

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (9)..(1118)

<400> 15

agcctcgg atg ctg gcc cgg agg aag ccg atg ctg ccg gcg ctc acc atc 50

Met Leu Ala Arg Arg Lys Pro Met Leu Pro Ala Leu Thr Ile

1

5

10

aac cct acc atc gcc gag ggc ccg tcc cca acc agc gag ggc gcc tcc 98

Asn Pro Thr Ile Ala Glu Gly Pro Ser Pro Thr Ser Glu Gly Ala Ser

15

20

25

30

gag gca aac ctg gtg gac ctg cag aag aag ctg gag gag ctg gaa ctt 146

Glu Ala Asn Leu Val Asp Leu Gln Lys Lys Leu Glu Glu Leu Glu Leu

35

40

45

gac gag cag cag aag ccg ctg gaa gcc ttt ctc acc cag aaa gcc aag 194

Asp Glu Gln Gln Lys Arg Leu Glu Ala Phe Leu Thr Gln Lys Ala Lys

50

55

60

gtc ggc gaa ctc aaa gac gat gac ttc gaa agg acc tca gag ctg gac 242

Val Gly Glu Leu Lys Asp Asp Asp Phe Glu Arg Thr Ser Glu Leu Asp

65

70

75

gcg ggc aac ggc ggg gtg gtc acc aaa gtc cag cac aga ccc tcg ggc 290

Ala Gly Asn Gly Gly Val Val Thr Lys Val Gln His Arg Pro Ser Gly

80

85

90

ctc atc atg gcc agg aag ctg atc cac ctt gag atc aag ccg gcc atc 338

Leu Ile Met Ala Arg Lys Leu Ile His Leu Glu Ile Lys Pro Ala Ile

95

100

105

110

cgg aac cag atc atc cgc gag cac cag gtc ctg cac gag tgc aac tca 386

Arg Asn Gln Ile Ile Arg Glu His Gln Val Leu His Glu Cys Asn Ser

115

120

125

ccg tac atc gtg ggc ttc tac ggg gcc ttc tac tgt gac agg gag atc 434

Pro Tyr Ile Val Gly Phe Tyr Gly Ala Phe Tyr Cys Asp Arg Glu Ile

130

135

140

agc atc tgc atg gag cac atg gat ggc ggc tcc ctg gac cag ggg ctg 482

Ser Ile Cys Met Glu His Met Asp Gly Gly Ser Leu Asp Gln Gly Leu

145

150

155

aaa gag gcc aag agg att ccc gag gac atc ctg ggg aaa gtc agc att 530

Lys Glu Ala Lys Arg Ile Pro Glu Asp Ile Leu Gly Lys Val Ser Ile

160

165

170

gcg gtt ctc cgg ggc ttg gcg tac ctc cga gag aag cac cag atc atg 578

Ala Val Leu Arg Gly Leu Ala Tyr Leu Arg Glu Lys His Gln Ile Met

175

180

185

190

cac cga aat gtg aag ccc tcc aac atc ctc gtg aac tct aga ggg gag 626

His Arg Asn Val Lys Pro Ser Asn Ile Leu Val Asn Ser Arg Gly Glu

195

200

205

atc aag ctg tgt gac ttc ggg gtg agc ggc cag ctc atc gac tcc atg	674
Ile Lys Leu Cys Asp Phe Gly Val Ser Gly Gln Leu Ile Asp Ser Met	
210 215 220	
gcc aac tcc ttc gtg ggc acg cgc tcc tac atg gct ccg gag cgg ttg	722
Ala Asn Ser Phe Val Gly Thr Arg Ser Tyr Met Ala Pro Glu Arg Leu	
225 230 235	
cag ggc aca cat tac tcg gtg cag tcg gtc atc tgg agc atg gac ctg	770
Gln Gly Thr His Tyr Ser Val Gln Ser Val Ile Trp Ser Met Asp Leu	
240 245 250	
tcc ctg gtg gag ctg gcc atc gaa agg tac ccc atc ccc ccg ccc gac	818
Ser Leu Val Glu Leu Ala Ile Glu Arg Tyr Pro Ile Pro Pro Pro Asp	
255 260 265 270	
gcc aag gag ctg gag gcc atc ttt ggc cag ccc gtg gtc gac agg gaa	866
Ala Lys Glu Leu Glu Ala Ile Phe Gly Gln Pro Val Val Asp Arg Glu	
275 280 285	
gaa gga gag cct cac agc atc tcc tct tgg cca ggg tcc ccc ggg cgc	914
Glu Gly Glu Pro His Ser Ile Ser Ser Trp Pro Gly Ser Pro Gly Arg	
290 295 300	
ccc aac agc ggt tac ggg atg gac agc ctg ccc gcc atg gcc atc ttc	962
Pro Asn Ser Gly Tyr Gly Met Asp Ser Leu Pro Ala Met Ala Ile Phe	
305 310 315	
gaa ctg ctg gac tat att gtg aaa gag ccg cct cct aag ctg ccc aac	1010
Glu Leu Leu Asp Tyr Ile Val Lys Glu Pro Pro Pro Lys Leu Pro Asn	
320 325 330	
ggg gtg ttc acc ccc gac ttc cag gag ttt gtc aat aaa tgc ctc atc	1058
Gly Val Phe Thr Pro Asp Phe Gln Glu Phe Val Asn Lys Cys Leu Ile	
335 340 345 350	
aaa aac cca acg gag cgg gcg gac cta aag atg ctc agt gag gtc att	1106
Lys Asn Pro Thr Glu Arg Ala Asp Leu Lys Met Leu Ser Glu Val Ile	
355 360 365	
cca tgt ata tga atata	1123
Pro Cys Ile	
370	

<210> 16
 <211> 369
 <212> PRT
 <213> Homo sapiens

<400> 16
 Met Leu Ala Arg Arg Lys Pro Met Leu Pro Ala Leu Thr Ile Asn Pro
 1 5 10 15
 Thr Ile Ala Glu Gly Pro Ser Pro Thr Ser Glu Gly Ala Ser Glu Ala
 20 25 30
 Asn Leu Val Asp Leu Gln Lys Lys Leu Glu Glu Leu Glu Leu Asp Glu

acagagagca ggagcttcaa ctacattgaa ttccattgta gcatggacgg gtatgttgat 420
agcatagaag acctaaagat ggtagaacct atcgggaact agaaagtcta tgcacatcct 480
caggtattgg tagagtattc agtgctttct aagtagcagc ccctgcctcc atcaat 536

<210> 18
<211> 537
<212> DNA
<213> Homo sapiens

<400> 18
ggcggcccg gtgactgaga tggcatcatc tctaaagatc tggggcacac tcttggccct 60
actttgcatc ctatgcacac tgcttgtaga gagcaaagaa gtttcttggg gagaattcat 120
gaaacagcac tacttaagtc caagtcgaga attcagagag tacaaatgtg atgtcctcat 180
gagagaaaaat gaagctctga aagacaagag ctctcacatg tttatctata tctcatggta 240
caaaatcgag catatatgca ctagtgcaca ctggatggat cgcttcgaa atgcatatgt 300
atgggtccag aatcctctca aagtactcaa gtgtcaccag gagaattcca aaaatagcta 360
cacagagagc aggagcttca actacattga attccattgt agcatggacg ggtatgttga 420
tagcatagaa gacctaaaga tggtagaacc tatcggcaac tagaaagtct atgcacatcc 480
tcaggtattg gtagagtatt cagtgccttc taagtagcag ccctgcctc catcaat 537

<210> 19
<211> 249
<212> DNA
<213> Homo sapiens

<400> 19
gaaatgcata tgtatgggtc cagatcctct caaagtactc aagtgtcacc aggagaattc 60
caaaaatagc tacacagaga gcaggagctt caactacatt gaattccatt gtagcatgga 120
cgggtatggt gatagcatag aagacctaaa gatggtagaa cctatcggca actagaaagt 180
ctatgcacat cctcaggtat tggtagagta ttcagtgcct tctaagtagc agccccctgc 240
tccatcaat 249

<210> 20
<211> 250
<212> DNA
<213> Homo sapiens

<400> 20
gaaatgcata tgtatgggcc ccaggtgccc tcaaagtact cgagtgtcac tgggagaagt 60
acaacaatag gtacacagag agcagaagct tcagctacat tgaattccat tgtggcgtag 120
atggatatgt tgataacata gaagacctga ggattataga acctatcagc aactagaaaag 180
tctatgcaca tcctcagata ttggtagagt attcagtgc tccaaagtgg tgggccctgc 240
ctccatcaat 250

<210> 21
<211> 419
<212> DNA
<213> Homo sapiens

<400> 21
ggtgactgag atggcatcct ctctgaagat ctggggcagt cccttggccc tgctttgcat 60
tctttgcagg ctacttgtag acagcaagga cgtttcctgg agagaattca tgaccctgca 120
ctatttagat ccaagccaag attttgaaga gtacaaatgt gatgtcctca tgagagaaaa 180

agaagctctg aaacgcaaga gctctcatat gtccatctat agcttatggc acaaaatgga 240
 gtgtatatgc attattgaaa tgggaataac cgatatagat atgcctatgt atgggcccag 300
 ggtgccctca aagtactcga gtgtcagtgg cagaagtact gcaatagcta cacagagatc 360
 ttcaactaca ttgaattcca ctgtggcaag gatgggtatg ttgatagcat agaagacct 419

<210> 22
 <211> 426
 <212> DNA
 <213> Homo sapiens

<400> 22
 ggtgactgag atgacatcct ctctaaagat ttggggcata ctcttgcccc tgctttgcat 60
 cctttgcagg ctgtgtgtat acagtaacaa catttactgg agagaattca taaaacttca 120
 ttacttaagt ccaagtcgag aattcaaaga gtacaaatgt gatgtcctca tgagagaaaa 180
 agaggctctg aaaggcaaga gctttcatat gttcatctat agcttatggg tcaaaattca 240
 gcgtgcatgc atcaatgaga aggggagcga ccgatataga aatgcatatg tatgggcccc 300
 aggtgccctc aaagtactcg agtgtcactg ggagaagtac aacaataggc acacagagag 360
 cagaagcttc agctacattg aattccattg tggcgtagat ggatatgttg ataacataga 420
 agacct 426

<210> 23
 <211> 256
 <212> DNA
 <213> Homo sapiens

<400> 23
 gccccggtga ctgagatggc atcctctctg aagatctggg gcagtccttt ggccctgctt 60
 tgcattcttt gcaggctact tgtacacagc aaggacgttt cctggagaga attcatgacc 120
 ctgcactatt tagatccaag ccaagatfff gaagagtaca aatgtgatgt cctcatgaga 180
 gaaaaagaag ctctgaaacg caagagctct catatgtcca tctatagctt atggcacaaa 240
 atggagtgtg tatgca 256

<210> 24
 <211> 256
 <212> DNA
 <213> Homo sapiens

<400> 24
 gccccggtga ctgagatggc atcatctcta aagatctggg gcacactctt ggccctactt 60
 tgcactctat gcacactgct tgtacagagc aaagaagttt cttggagaga attcatgaaa 120
 cagcactact taagtccaag tgcagaattc agagagtaca aatgtgatgt cctcatgaga 180
 gaaaatgaag ctctgaaaga caagagctct cacatgttta tctatatctc atggtacaaa 240
 atcgagcata tatgca 256

<210> 25
 <211> 61
 <212> DNA
 <213> Homo sapiens

<400> 25
 cttcaactac attgaattcc actgtggcaa ggatgggtat gttgatagca tagaagacct 60
 a 61

<210> 26
 <211> 61
 <212> DNA
 <213> Homo sapiens

<400> 26
 cttcaactac attgaattcc attgtagcat ggacgggtat gttgatagca tagaagacct 60
 a 61

<210> 27
 <211> 126
 <212> PRT
 <213> Homo sapiens

<400> 27
 Met Ala Ser Ser Leu Lys Ile Trp Gly Ser Pro Leu Ala Leu Leu Cys
 1 5 10 15
 Ile Leu Cys Arg Leu Leu Val His Ser Lys Asp Val Ser Trp Arg Glu
 20 25 30
 Phe Met Thr Leu His Tyr Leu Asp Pro Ser Gln Asp Phe Glu Glu Tyr
 35 40 45
 Lys Cys Asp Val Leu Met Arg Glu Lys Glu Ala Leu Lys Arg Lys Ser
 50 55 60
 Ser His Met Ser Ile Tyr Ser Leu Trp His Lys Met Glu Cys Ile Cys
 65 70 75 80
 Ile Ile Glu Met Gly Ile Thr Asp Ile Asp Met Pro Met Tyr Gly Pro
 85 90 95
 Arg Val Pro Ser Lys Tyr Ser Ser Val Ser Gly Arg Ser Thr Ala Ile
 100 105 110
 Ala Thr Gln Arg Ser Ser Thr Thr Leu Asn Ser Thr Val Ala
 115 120 125

<210> 28
 <211> 128
 <212> PRT
 <213> Homo sapiens

<400> 28
 Met Thr Ser Ser Leu Lys Ile Trp Gly Ile Leu Leu Ala Leu Leu Cys
 1 5 10 15
 Ile Leu Cys Arg Leu Cys Val Tyr Ser Asn Asn Ile Tyr Trp Arg Glu
 20 25 30
 Phe Ile Lys Leu His Tyr Leu Ser Pro Ser Arg Glu Phe Lys Glu Tyr
 35 40 45

Lys Cys Asp Val Leu Met Arg Glu Lys Glu Ala Leu Lys Gly Lys Ser
 50 55 60
 Phe His Thr Phe Ile Tyr Ser Leu Trp Phe Lys Ile Gln Arg Ala Cys
 65 70 75 80
 Ile Asn Glu Lys Gly Ser Asp Arg Tyr Arg Asn Ala Tyr Val Trp Pro
 85 90 95
 Gln Val Pro Ser Asn Tyr Ser Ser Val Thr Gly Arg Ser Thr Thr Ile
 100 105 110
 Gly Thr Gln Arg Ala Glu Ala Ser Ala Thr Leu Asn Ser Ile Val Ala
 115 120 125

<210> 29
 <211> 147
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)..(147)
 <223> Wherein Xaa is any amino acid as defined in the
 specification

<400> 29
 Met Ala Ser Ser Leu Lys Ile Trp Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1 5 10 15
 Xaa Xaa Xaa Xaa Xaa Xaa Val Gln Ser Lys Glu Val Ser Trp Arg Glu
 20 25 30
 Phe Met Lys Gln His Tyr Leu Ser Pro Ser Arg Glu Phe Arg Glu Tyr
 35 40 45
 Lys Cys Asp Val Leu Met Arg Glu Asn Glu Ala Leu Lys Asp Lys Ser
 50 55 60
 Ser His Met Phe Ile Tyr Ile Ser Trp Tyr Lys Ile Glu His Ile Cys
 65 70 75 80
 Thr Ser Asp Asn Trp Met Asp Arg Phe Arg Asn Ala Tyr Val Trp Val
 85 90 95
 Gln Asn Pro Leu Lys Val Leu Lys Cys His Gln Glu Asn Ser Lys Asn
 100 105 110
 Ser Tyr Thr Glu Ser Arg Ser Phe Asn Tyr Ile Glu Phe His Cys Ser
 115 120 125
 Met Asp Gly Tyr Val Asp Ser Ile Glu Asp Leu Lys Met Val Glu Pro
 130 135 140

Ile Gly Asn
145

<210> 30
<211> 147
<212> PRT
<213> Homo sapiens

<400> 30
Met Ala Ser Ser Leu Lys Ile Trp Gly Thr Leu Leu Ala Leu Leu Cys
1 5 10 15
Ile Leu Cys Thr Leu Leu Val Gln Ser Lys Glu Val Ser Trp Arg Glu
20 25 30
Phe Met Lys Gln His Tyr Leu Ser Pro Ser Arg Glu Phe Arg Glu Tyr
35 40 45
Lys Cys Asp Val Leu Met Arg Glu Asn Glu Ala Leu Lys Asp Lys Ser
50 55 60
Ser His Met Phe Ile Tyr Ile Ser Trp Tyr Lys Ile Glu His Ile Cys
65 70 75 80
Thr Ser Asp Asn Trp Met Asp Arg Phe Arg Asn Ala Tyr Val Trp Val
85 90 95
Gln Asn Pro Leu Lys Val Leu Lys Cys His Gln Glu Asn Ser Lys Asn
100 105 110
Ser Tyr Thr Glu Ser Arg Ser Phe Asn Tyr Ile Glu Phe His Cys Ser
115 120 125
Met Asp Gly Tyr Val Asp Ser Ile Glu Asp Leu Lys Met Val Glu Pro
130 135 140
Ile Gly Asn
145

<210> 31
<211> 147
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)..(147)
<223> Wherein Xaa is any amino acid as defined in the
specification

<400> 31
Met Ala Ser Ser Leu Lys Ile Trp Gly Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Val Gln Ser Lys Glu Val Ser Trp Arg Glu
 20 25 30
 Phe Met Lys Gln His Tyr Leu Ser Pro Ser Arg Glu Phe Arg Glu Tyr
 35 40 45
 Lys Cys Asp Val Leu Met Arg Glu Asn Glu Ala Leu Lys Asp Lys Ser
 50 55 60
 Ser His Met Phe Ile Tyr Ile Ser Trp Tyr Lys Ile Glu His Ile Cys
 65 70 75 80
 Thr Ser Asp Asn Trp Met Asp Arg Phe Arg Asn Ala Tyr Val Trp Val
 85 90 95
 Gln Asn Pro Leu Lys Val Leu Lys Cys His Gln Glu Asn Ser Lys Asn
 100 105 110
 Ser Tyr Thr Glu Ser Arg Ser Phe Asn Tyr Ile Glu Phe His Cys Ser
 115 120 125
 Met Asp Gly Tyr Val Asp Ser Ile Glu Asp Leu Lys Met Val Glu Pro
 130 135 140
 Ile Gly Asn
 145

<210> 32
 <211> 147
 <212> PRT
 <213> Homo sapiens

<400> 32
 Met Thr Ser Ser Leu Lys Ile Trp Gly Ile Leu Leu Ala Leu Leu Cys
 1 5 10 15
 Ile Leu Cys Arg Leu Cys Val Tyr Ser Asn Asn Ile Tyr Trp Arg Glu
 20 25 30
 Phe Ile Lys Leu His Tyr Leu Ser Pro Ser Arg Glu Phe Lys Glu Tyr
 35 40 45
 Lys Cys Asp Val Leu Met Arg Glu Lys Glu Ala Leu Lys Gly Lys Ser
 50 55 60
 Phe His Met Phe Ile Tyr Ser Leu Trp Phe Lys Ile Gln Arg Ala Cys
 65 70 75 80
 Ile Asn Glu Lys Gly Ser Asp Arg Tyr Arg Asn Ala Tyr Val Trp Ala
 85 90 95
 Pro Gly Ala Leu Lys Val Leu Glu Cys His Trp Glu Lys Tyr Asn Asn
 100 105 110
 Arg Tyr Thr Glu Ser Arg Ser Phe Ser Tyr Ile Glu Phe His Cys Gly
 115 120 125

Val Asp Gly Tyr Val Asp Asn Ile Glu Asp Leu Arg Ile Ile Glu Pro
 130 135 140

Ile Ser Asn
 145

<210> 33
 <211> 394
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)..(394)
 <223> Wherein Xaa is any amino acid as defined in the
 specification

<400> 33
 Met Leu Ala Arg Arg Lys Pro Met Leu Pro Ala Leu Thr Ile Asn Pro
 1 5 10 15

Thr Ile Ala Glu Gly Pro Ser Pro Thr Ser Glu Gly Ala Ser Glu Ala
 20 25 30

Asn Leu Val Asp Leu Gln Lys Lys Leu Glu Glu Leu Glu Leu Asp Glu
 35 40 45

Gln Gln Lys Arg Leu Glu Ala Phe Leu Thr Gln Lys Ala Lys Val Gly
 50 55 60

Glu Leu Lys Asp Asp Asp Phe Glu Arg Thr Ser Glu Leu Asp Ala Gly
 65 70 75 80

Asn Gly Gly Val Val Thr Lys Val Gln His Arg Pro Ser Gly Leu Ile
 85 90 95

Met Ala Arg Lys Leu Ile His Leu Glu Ile Lys Pro Ala Ile Arg Asn
 100 105 110

Gln Ile Ile Arg Glu His Gln Val Leu His Glu Cys Asn Ser Pro Tyr
 115 120 125

Ile Val Gly Phe Tyr Gly Ala Phe Tyr Cys Asp Arg Glu Ile Ser Ile
 130 135 140

Cys Met Glu His Met Asp Gly Gly Ser Leu Asp Gln Gly Leu Lys Glu
 145 150 155 160

Ala Lys Arg Ile Pro Glu Asp Ile Leu Gly Lys Val Ser Ile Ala Val
 165 170 175

Leu Arg Gly Leu Ala Tyr Leu Arg Glu Lys His Gln Ile Met His Arg
 180 185 190

Asn Val Lys Pro Ser Asn Ile Leu Val Asn Ser Arg Gly Glu Ile Lys

195	200	205
Leu Cys Asp Phe Gly Val	Ser Gly Gln Leu Ile	Asp Ser Met Ala Asn
210	215	220
Ser Phe Val Gly Thr Arg	Ser Tyr Met Ala Pro	Glu Arg Leu Gln Gly
225	230	235 240
Thr His Tyr Ser Val Gln	Ser Val Ile Trp Ser	Met Asp Leu Ser Leu
245	250	255
Val Glu Leu Ala Ile Glu	Arg Tyr Pro Ile Pro	Pro Pro Asp Ala Lys
260	265	270
Glu Leu Glu Ala Ile Phe	Gly Gln Pro Val Val	Asp Arg Glu Glu Gly
275	280	285
Glu Pro His Ser Ile Ser	Ser Trp Pro Gly Ser	Pro Gly Arg Pro Asn
290	295	300
Ser Gly Tyr Gly Met Asp	Ser Leu Pro Ala Met	Ala Ile Phe Glu Leu
305	310	315 320
Leu Asp Tyr Ile Val Lys	Glu Pro Pro Pro Lys	Leu Pro Asn Gly Val
325	330	335
Phe Thr Pro Glu Phe Gln	Glu Phe Val Asn Lys	Cys Leu Ile Lys Asn
340	345	350
Pro Thr Glu Arg Ala Asp	Leu Lys Met Leu Thr	Asn His Ala Phe Ile
355	360	365
Lys Arg Ser Glu Val Lys	Glu Ala Asp Phe Ala	Cys Leu Cys Lys Thr
370	375	380
Leu Xaa Ala Glu Pro Ser	Pro Ala His Pro	
385	390	

<210> 34
 <211> 395
 <212> PRT
 <213> Homo sapiens

<400> 34
 Met Leu Ala Arg Arg Lys Pro Val Leu Pro Ala Leu Thr Ile Asn Pro
 1 5 10 15
 Thr Ile Ala Glu Gly Pro Ser Pro Thr Ser Glu Gly Ala Ser Glu Ala
 20 25 30
 Asn Leu Val Asp Leu Gln Lys Lys Leu Glu Glu Leu Glu Leu Asp Glu
 35 40 45
 Gln Gln Lys Lys Arg Leu Glu Ala Phe Leu Thr Gln Lys Ala Lys Val
 50 55 60

Gly	Glu	Leu	Lys	Asp	Asp	Asp	Phe	Glu	Arg	Ile	Ser	Glu	Leu	Gly	Ala	65	70	75	80
Gly	Asn	Gly	Gly	Val	Val	Thr	Lys	Val	Gln	His	Arg	Pro	Ser	Gly	Leu	85	90	95	
Ile	Met	Ala	Arg	Lys	Leu	Ile	His	Leu	Glu	Ile	Lys	Pro	Ala	Ile	Arg	100	105	110	
Asn	Gln	Ile	Ile	Arg	Glu	Leu	Gln	Val	Leu	His	Glu	Cys	Asn	Ser	Pro	115	120	125	
Tyr	Ile	Val	Gly	Phe	Tyr	Gly	Ala	Phe	Tyr	Ser	Asp	Gly	Glu	Ile	Ser	130	135	140	
Ile	Cys	Met	Glu	His	Met	Asp	Gly	Gly	Ser	Leu	Asp	Gln	Val	Leu	Lys	145	150	155	160
Glu	Ala	Lys	Arg	Ile	Pro	Glu	Glu	Ile	Leu	Gly	Lys	Val	Ser	Ile	Ala	165	170	175	
Val	Leu	Arg	Gly	Leu	Ala	Tyr	Leu	Arg	Glu	Lys	His	Gln	Ile	Met	His	180	185	190	
Arg	Asp	Val	Lys	Pro	Ser	Asn	Ile	Leu	Val	Asn	Ser	Arg	Gly	Glu	Ile	195	200	205	
Lys	Leu	Cys	Asp	Phe	Gly	Val	Ser	Gly	Gln	Leu	Ile	Asp	Ser	Met	Ala	210	215	220	
Asn	Ser	Phe	Val	Gly	Thr	Arg	Ser	Tyr	Met	Ala	Pro	Glu	Arg	Leu	Gln	225	230	235	240
Gly	Thr	His	Tyr	Ser	Val	Gln	Ser	Asp	Ile	Trp	Ser	Met	Gly	Leu	Ser	245	250	255	
Leu	Val	Glu	Leu	Ala	Val	Gly	Arg	Tyr	Pro	Ile	Pro	Pro	Pro	Asp	Ala	260	265	270	
Lys	Glu	Leu	Glu	Ala	Ile	Phe	Gly	Arg	Pro	Val	Val	Asp	Gly	Glu	Glu	275	280	285	
Gly	Glu	Pro	His	Ser	Ile	Ser	Pro	Arg	Pro	Arg	Pro	Pro	Gly	Arg	Pro	290	295	300	
Val	Ser	Gly	His	Gly	Met	Asp	Ser	Arg	Pro	Ala	Met	Ala	Ile	Phe	Glu	305	310	315	320
Leu	Leu	Asp	Tyr	Ile	Val	Asn	Glu	Pro	Pro	Pro	Lys	Leu	Pro	Asn	Gly	325	330	335	
Val	Phe	Thr	Pro	Asp	Phe	Gln	Glu	Phe	Val	Asn	Lys	Cys	Leu	Ile	Lys	340	345	350	
Asn	Pro	Ala	Glu	Arg	Ala	Asp	Leu	Lys	Met	Leu	Thr	Asn	His	Thr	Phe	355	360	365	

Ile Lys Arg Ser Glu Val Glu Glu Val Asp Phe Ala Gly Trp Leu Cys
 370 375 380

Lys Thr Leu Arg Leu Asn Gln Pro Gly Thr Pro
 385 390 395

<210> 35

<211> 392

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)..(392)

<223> Wherein Xaa is any amino acid as defined in the
 specification

<400> 35

Leu Ala Arg Arg Lys Pro Met Leu Pro Ala Leu Thr Ile Asn Pro Thr
 1 5 10 15

Ile Ala Glu Gly Pro Ser Pro Thr Ser Glu Gly Ala Ser Glu Ala Asn
 20 25 30

Leu Val Asp Leu Gln Lys Lys Leu Glu Glu Leu Glu Leu Asp Glu Gln
 35 40 45

Gln Lys Arg Leu Glu Ala Phe Leu Thr Gln Lys Ala Lys Val Gly Glu
 50 55 60

Leu Lys Asp Asp Asp Phe Glu Arg Thr Ser Glu Leu Asp Ala Gly Asn
 65 70 75 80

Gly Gly Val Val Thr Lys Val Gln His Arg Pro Ser Gly Leu Ile Met
 85 90 95

Ala Arg Lys Leu Ile His Leu Glu Ile Lys Pro Ala Ile Arg Asn Gln
 100 105 110

Ile Ile Arg Glu His Gln Val Leu His Glu Cys Asn Ser Pro Tyr Ile
 115 120 125

Val Gly Phe Tyr Gly Ala Phe Tyr Cys Asp Arg Glu Ile Ser Ile Cys
 130 135 140

Met Glu His Met Asp Gly Gly Ser Leu Asp Gln Gly Leu Lys Glu Ala
 145 150 155 160

Lys Arg Ile Pro Glu Asp Ile Leu Gly Lys Val Ser Ile Ala Val Leu
 165 170 175

Arg Gly Leu Ala Tyr Leu Arg Glu Lys His Gln Ile Met His Arg Asn
 180 185 190

Val Lys Pro Ser Asn Ile Leu Val Asn Ser Arg Gly Glu Ile Lys Leu
 195 200 205

Cys Asp Phe Gly Val Ser Gly Gln Leu Ile Asp Ser Met Ala Asn Ser
 210 215 220

Phe Val Gly Thr Arg Ser Tyr Met Ala Pro Glu Arg Leu Gln Gly Thr
 225 230 235 240

His Tyr Ser Val Gln Ser Val Ile Trp Ser Met Asp Leu Ser Leu Val
 245 250 255

Glu Leu Ala Ile Glu Arg Tyr Pro Ile Pro Pro Pro Asp Ala Lys Glu
 260 265 270

Leu Glu Ala Ile Phe Gly Gln Pro Val Val Asp Arg Glu Glu Gly Glu
 275 280 285

Pro His Ser Ile Ser Ser Trp Pro Gly Ser Pro Gly Arg Pro Asn Ser
 290 295 300

Gly Tyr Gly Met Asp Ser Leu Pro Ala Met Ala Ile Phe Glu Leu Leu
 305 310 315 320

Asp Tyr Ile Val Lys Glu Pro Pro Pro Lys Leu Pro Asn Gly Val Phe
 325 330 335

Thr Pro Glu Phe Gln Glu Phe Val Asn Lys Cys Leu Ile Lys Asn Pro
 340 345 350

Thr Glu Arg Ala Asp Leu Lys Met Leu Thr Asn His Ala Phe Ile Lys
 355 360 365

Arg Ser Glu Val Lys Glu Ala Asp Phe Ala Cys Leu Cys Lys Thr Leu
 370 375 380

Xaa Ala Glu Pro Ser Pro Ala His
 385 390

<210> 36
 <211> 389
 <212> PRT
 <213> Homo sapiens

<400> 36
 Met Pro Lys Lys Lys Pro Thr Pro Ile Gln Leu Asn Pro Ala Pro Asp
 1 5 10 15

Gly Ser Ala Val Asn Gly Thr Ser Ser Ala Glu Thr Asn Leu Glu Ala
 20 25 30

Leu Gln Lys Lys Leu Glu Glu Leu Glu Leu Asp Glu Gln Gln Arg Lys
 35 40 45

Arg Leu Glu Ala Phe Leu Thr Gln Lys Gln Lys Val Gly Glu Leu Lys
 50 55 60

Asp Asp Asp Phe Glu Lys Ile Ser Glu Leu Gly Ala Gly Asn Gly Gly

65		70		75		80
Val Val Phe Lys Val Ser His Lys Pro Ser Gly Leu Val Met Ala Arg						
	85		90		95	
Lys Leu Ile His Leu Glu Ile Lys Pro Ala Ile Arg Asn Gln Ile Ile						
	100		105		110	
Arg Glu Leu Gln Val Leu His Glu Cys Asn Ser Pro Tyr Ile Val Gly						
	115		120		125	
Phe Tyr Gly Ala Phe Tyr Ser Asp Gly Glu Ile Ser Ile Cys Met Glu						
	130		135		140	
His Met Asp Gly Gly Ser Leu Asp Gln Val Leu Lys Lys Ala Gly Arg						
	145		150		155	
Ile Pro Glu Gln Ile Leu Gly Lys Val Ser Ile Ala Val Ile Lys Gly						
	165		170		175	
Leu Thr Tyr Leu Arg Glu Lys His Lys Ile Met His Arg Asp Val Lys						
	180		185		190	
Pro Ser Asn Ile Leu Val Asn Ser Arg Gly Glu Ile Lys Leu Cys Asp						
	195		200		205	
Phe Gly Val Ser Gly Gln Leu Ile Asp Ser Met Ala Asn Ser Phe Val						
	210		215		220	
Gly Thr Arg Ser Tyr Met Ser Pro Glu Arg Leu Gln Gly Thr His Tyr						
	225		230		235	
Ser Val Gln Ser Asp Ile Trp Ser Met Gly Leu Ser Leu Val Glu Met						
	245		250		255	
Ala Val Gly Arg Tyr Pro Ile Pro Pro Pro Asp Ala Lys Glu Leu Glu						
	260		265		270	
Leu Met Phe Gly Cys Gln Val Glu Gly Asp Ala Ala Glu Thr Pro Pro						
	275		280		285	
Arg Pro Arg Thr Pro Gly Arg Pro Leu Ser Ser Tyr Gly Met Asp Ser						
	290		295		300	
Arg Pro Pro Met Ala Ile Phe Glu Leu Leu Asp Tyr Ile Val Asn Glu						
	305		310		315	
Pro Pro Pro Lys Leu Pro Ser Gly Val Phe Ser Leu Glu Phe Gln Asp						
	325		330		335	
Phe Val Asn Lys Cys Leu Ile Lys Asn Pro Ala Glu Arg Ala Asp Leu						
	340		345		350	
Lys Gln Leu Met Val His Ala Phe Ile Lys Arg Ser Asp Ala Glu Glu						
	355		360		365	
Val Asp Phe Ala Gly Trp Leu Cys Ser Thr Ile Gly Leu Asn Gln Pro						

370

375

380

Ser Thr Pro Thr His

385

<210> 37

<211> 224

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)..(224)

<223> Wherein Xaa is any amino acid as defined in the
specification

<400> 37

Gly	Lys	Val	Ser	Ile	Ala	Val	Leu	Arg	Gly	Leu	Ala	Tyr	Leu	Arg	Glu
1				5					10					15	

Lys	His	Gln	Ile	Met	His	Arg	Asn	Val	Lys	Pro	Ser	Asn	Ile	Leu	Val
		20					25						30		

Asn	Ser	Arg	Gly	Glu	Ile	Lys	Leu	Cys	Asp	Phe	Gly	Val	Ser	Gly	Gln
		35					40					45			

Leu	Ile	Asp	Ser	Met	Ala	Asn	Ser	Phe	Val	Gly	Thr	Arg	Ser	Tyr	Met
	50					55					60				

Ala	Pro	Glu	Arg	Leu	Gln	Gly	Thr	His	Tyr	Ser	Val	Gln	Ser	Val	Ile
65					70					75					80

Trp	Ser	Met	Asp	Leu	Ser	Leu	Val	Glu	Leu	Ala	Ile	Glu	Arg	Tyr	Pro
		85							90					95	

Ile	Pro	Pro	Pro	Asp	Ala	Lys	Glu	Leu	Glu	Ala	Ile	Phe	Gly	Gln	Pro
		100						105					110		

Val	Val	Asp	Arg	Glu	Glu	Gly	Glu	Pro	His	Ser	Ile	Ser	Ser	Trp	Pro
		115					120					125			

Gly	Ser	Pro	Gly	Arg	Pro	Asn	Ser	Gly	Tyr	Gly	Met	Asp	Ser	Leu	Pro
		130				135					140				

Ala	Met	Ala	Ile	Phe	Glu	Leu	Leu	Asp	Tyr	Ile	Val	Lys	Glu	Pro	Pro
145					150					155					160

Pro	Lys	Leu	Pro	Asn	Gly	Val	Phe	Thr	Pro	Glu	Phe	Gln	Glu	Phe	Val
			165						170					175	

Asn	Lys	Cys	Leu	Ile	Lys	Asn	Pro	Thr	Glu	Arg	Ala	Asp	Leu	Lys	Met
			180					185					190		

Leu	Thr	Asn	His	Ala	Phe	Ile	Lys	Arg	Ser	Glu	Val	Lys	Glu	Ala	Asp
		195					200					205			

Phe Ala Cys Leu Cys Lys Thr Leu Xaa Ala Glu Pro Ser Pro Ala His
 210 215 220

<210> 38
 <211> 228
 <212> PRT
 <213> Homo sapiens

<400> 38
 Gly Glu Ile Ser Ile Cys Met Glu His Met Val Ile Lys Gly Leu Thr
 1 5 10 15
 Tyr Leu Arg Glu Lys His Lys Ile Met His Arg Asp Val Lys Pro Ser
 20 25 30
 Asn Ile Leu Val Asn Ser Arg Gly Glu Ile Lys Leu Cys Asp Phe Gly
 35 40 45
 Val Ser Gly Gln Leu Ile Asp Ser Met Ala Asn Ser Phe Val Gly Thr
 50 55 60
 Arg Ser Tyr Met Ser Pro Glu Arg Leu Gln Gly Thr His Tyr Ser Val
 65 70 75 80
 Gln Ser Asp Ile Trp Ser Met Gly Leu Ser Leu Val Glu Met Ala Val
 85 90 95
 Gly Arg Tyr Pro Ile Pro Pro Pro Asp Ala Lys Glu Leu Glu Leu Met
 100 105 110
 Phe Gly Cys Gln Val Glu Gly Asp Ala Ala Glu Thr Pro Pro Arg Pro
 115 120 125
 Arg Thr Thr Pro Gly Arg Pro Leu Ser Ser Tyr Gly Met Asp Ser Arg
 130 135 140
 Pro Pro Met Ala Ile Phe Gln Leu Leu Asp Tyr Ile Val Asn Glu Pro
 145 150 155 160
 Pro Pro Lys Leu Pro Ser Gly Val Phe Ser Leu Glu Phe Gln Asp Phe
 165 170 175
 Val Asn Lys Cys Leu Ile Lys Asn Pro Ala Glu Arg Ala Asp Leu Lys
 180 185 190
 Gln Leu Met Val His Ala Phe Ile Lys Arg Ser Asp Ala Glu Glu Val
 195 200 205
 Asp Phe Ala Gly Trp Leu Cys Ser Thr Ile Gly Leu Asn Gln Pro Ser
 210 215 220
 Thr Pro Thr His
 225

<210> 39
 <211> 2096
 <212> DNA
 <213> Homo sapiens

<400> 39
 gaaggtgcca ctatattaaa aggataaaga aaattcagat aaaatacgag caggaagcat 60
 atgataatgg ctcttatata tccatacagt cccaaagaac atctgctgtc tttggcgag 120
 ggccataatat ttgtgggttc aggtgcccct aaagtgtcta taggagccta taaacaaagc 180
 ctataaactg tgttgtagga aagacagcac atattgttac aggctcatac aaagaaaata 240
 tatgtagtgt ttcagtctag ttcttacctt cctaagtaga gtccttacac atgtgtaagg 300
 gagataggta ttgagaaagg gagagtggga atgtgaagtg atgcataaca tgcaacttag 360
 taggaatttt gacctgtgtt gggcacagct tgacaagctt gtgtgtgtgt atcaccacat 420
 accctcactt ccccttccc tacctctttc tcttactga cttcaaggga gagcatataa 480
 atgacatcaa ggggtatgaa aagccactta actgcagact tgtaggcagc aactcaccct 540
 caagaggaag tcttcaggct ctagaaacat ctttaacttc ggcttctgca ccataagcct 600
 cagactcaat gccaccctgc agctgtgcca gatcactttg tgccttcagc gtgctgctgt 660
 tgactgttct gggttcctcc accaatggac aaactaagag aaacataggg aaaaggaaat 720
 gtagagatct gttccttgca cctgttgctg cttctgctat acctgtatct gggagaaaga 780
 ctggcttggt gtcctgggg ctggagagtg ccattataac aacaaatcca aatggagggg 840
 tcacagagag ggggcacttc acatttgcgt ggcattctgc tgggcacttt aataaagctt 900
 tacagatcat attcacaatg gctttatgag agaggtaaca ttaccttcaa tttacaattg 960
 agagaactga gaaaaatatt caccgacct aatagatcac tttttacccc agctgtaagt 1020
 gtagacagtg acttgtagac tgaactgcgc tgcgtgtatg tgaagtcaac ctttgtactt 1080
 catcccagaa acatccacaa tttggagttg gtctcagcag gacccattg cagcaaagac 1140
 gaagtaatgt aagccactgc ttctgtgcta tgcctcatc aggggaagccc tctacctcca 1200
 tccccatctg cattcatttc ctccagtctc acagatcctt tctgatattc aggccaggac 1260
 acccacagat aattctatct tctcttgtag agccactctg taagatggga gaaaaaatct 1320
 gcctggaccc agatgctccc agaatacaata aaattgtaca gaaaatggtg aaagttgatg 1380
 aattcatctg gttaatttgt taactttctg ctaacgcttt tcaactggaag gggaggattt 1440
 tgaagtcttg actttctcag attcttattt atccaggata cttattctta ctgtattaaa 1500
 attttgatct aagttctatt ctgtttcaaa aatctcattt tattctgaga atgctggata 1560
 aaagataaca gaaagaagg gaaaataagc aagccatgct tcaatatata atatatgttt 1620
 tcccccaat ccttggttaa acattgtagt gcactttccc tttatttatt tgaaaatttc 1680
 tattgaaaca catctttgtt gatttttcca accccactct actgtaagac tagacatgct 1740
 gatgataata aacagattta ataattggtt atgatattag gaatcacaca gagcccagcg 1800
 caaaataactt gctcaataaa tttttgttag tatgttcagg aacttaatag ggtcttttag 1860
 tgtcttagtg ctattatgtc ttgcttaaaa catcttctga aagtttcttc tgatgtttgt 1920
 ttttagccttc aaaccctaaa aataataaag ttgtagaatg taagtcttgt gaactctgct 1980
 tttttacttt aaagtgtata tatttaccct tggtagaata aaaaatagat gatggaaatg 2040
 aattaatgta tcccattaaa aaacctgtga tattttttga aacaagaaag aaagaa 2096

<210> 40
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 40
 Pro Pro Cys Ser Cys Ala Arg Ser Leu Cys Ala Leu Gln Val Leu Leu
 1 5 10 15
 Leu Thr Val Leu Gly Ser Ser Thr Asn Gly Gln Thr Lys Arg Asn Ile
 20 25 30

Gly Lys Ser Val Asp Ser Asp Leu Tyr Thr Glu Leu Arg Cys Val Tyr
 35 40 45
 Val Lys Ser Thr Phe Val Leu His Pro Arg Asn Ile His Asn Leu Glu
 50 55 60
 Leu Val Ser Ala Gly Pro His Cys Ser Lys Asp Glu Glu Lys Ile Cys
 65 70 75 80
 Leu Asp Pro Asp Ala Pro Arg Ile Asn Lys Ile Val Gln Lys Met Leu
 85 90 95
 Lys Val Asp Glu
 100

<210> 41
 <211> 117
 <212> PRT
 <213> Homo sapiens

<400> 41
 Pro Ser Cys Asn Ser Ala Arg Pro Leu His Ala Leu Gln Val Leu Leu
 1 5 10 15
 Leu Leu Ser Leu Leu Leu Thr Ala Leu Ala Ser Ser Thr Lys Gly Gln
 20 25 30
 Thr Lys Arg Asn Leu Ala Lys Gly Lys Glu Glu Ser Leu Asp Ser Asp
 35 40 45
 Leu Tyr Ala Glu Leu Arg Cys Met Cys Ile Lys Thr Thr Ser Gly Ile
 50 55 60
 His Pro Lys Asn Ile Gln Ser Leu Glu Val Ile Gly Lys Gly Thr His
 65 70 75 80
 Cys Asn Gln Val Glu Val Ile Ala Thr Leu Lys Asp Gly Arg Lys Ile
 85 90 95
 Cys Leu Asp Pro Asp Ala Pro Arg Ile Lys Lys Ile Val Gln Lys Lys
 100 105 110
 Leu Ala Gly Asp Glu
 115

<210> 42
 <211> 52
 <212> PRT
 <213> Homo sapiens

<400> 42
 Lys Ser Val Asp Ser Asp Leu Tyr Thr Glu Leu Arg Cys Val Tyr Val
 1 5 10 15
 Lys Ser Thr Phe Val Leu His Pro Arg Asn Ile His Asn Leu Glu Leu

20 25 30

Val Ser Ala Gly Pro His Cys Ser Lys Asp Glu Glu Lys Ile Cys Leu
35 40 45

Asp Pro Asp Ala
50

<210> 43
<211> 60
<212> PRT
<213> Homo sapiens

<400> 43
Arg Ala Ala Gly Ala Ser Val Ala Thr Glu Leu Arg Cys Gln Cys Leu
1 5 10 15

Gln Thr Leu Gln Gly Ile His Pro Lys Asn Ile Gln Ser Val Asn Val
20 25 30

Lys Ser Pro Gly Pro His Cys Ala Gln Thr Glu Val Ile Ala Thr Leu
35 40 45

Lys Asn Gly Arg Lys Ala Cys Leu Asn Pro Ala Ser
50 55 60

<210> 44
<211> 60
<212> PRT
<213> Homo sapiens

<400> 44
Arg Ala Ala Gly Ala Pro Leu Ala Thr Glu Leu Arg Cys Gln Cys Leu
1 5 10 15

Gln Thr Leu Gln Gly Ile His Leu Lys Asn Ile Gln Ser Val Lys Val
20 25 30

Lys Ser Pro Gly Pro His Cys Ala Gln Thr Glu Val Ile Ala Thr Leu
35 40 45

Lys Asn Gly Gln Lys Ala Cys Leu Asn Pro Ala Ser
50 55 60

<210> 45
<211> 53
<212> PRT
<213> Homo sapiens

<400> 45
His Val Glu Leu Arg Cys Leu Cys Leu Asn Thr Val Ser Gly Ile His
1 5 10 15

Pro Ser Asn Ile Gln Ser Leu Glu Val Ile Arg Ala Gly Ala His Cys

20

25

30

Ala Lys Val Glu Val Ile Ala Thr Leu Lys Asn Asp Asp Lys Ile Cys
 35 40 45

Leu Asp Pro Glu Ala
 50

<210> 46
 <211> 41100
 <212> DNA
 <213> Homo sapiens

<220>
 <223> GENOMIC DNA

<400> 46
 taagggttgt cgttctcctt cctgatgata agggaggaga gacgcaggga gacatctact 60
 tccaagtaa atcctatagt atgggacact gaggtttcag gcaaagtgtt aaatgttctc 120
 ctgatttgta tccaacttaa acctgatgtc ctgtagccct ggaagagaca ataccctta 180
 aagctagagg cacaaagagg gatccaacca ttaatagcta agtttttgca attcgggttg 240
 ttaaacctct gtgagtcctg ttgtaataca ccaatcgta cagttaaaaa accaaatgga 300
 caccatagat ttggtcaaga acttcaagct ttcaatgagg ctgtcattcc catacatcct 360
 atagtgccca atccctacgt gctgttagcc tgggtcccat cctggggat gccaatgtgt 420
 ttacagagtt agatcttaaa gatgtctttt tgtttttttt ttttttggtt tttgtttttt 480
 ttggcattgc agtactccct gattcacaat tcatcttggc ttttgaatgg attgatcctg 540
 acagtcaattt ggtttatcaa tgaacttgga cagttcttcc ccagggtattt aggggcagcc 600
 cttatctggt tggaaatgca ttggctagag aattaaggat gttacactta aataggggca 660
 ttattatcca atatgtggat gatgtgttgg ttgctagccc aacaaaaaga aacttggacg 720
 aaaatacctt taagttgcta aattttctgg gagctaattg gtatagggtc tcacagcaga 780
 gggccagat ttcaactcaa gaggctaaat acttaggata tgcctaacc cctggcacc 840
 aggcaatagt accagaacaa aaggaaagcta tcttgggcat tccaaaacc caaactagaa 900
 agcagctgag agcttttcta gcagtgtcag gattggggca tatgggtcaag cctttatatg 960
 atgccctgaa aggagcgaat gtagattctt tagaatggaa tagcaattgt aaacaagctt 1020
 ttaatgcttt caaggaaaaa ttgggatcag ctccagtcct acggatccct aattttgata 1080
 agccattttt ctcttatgtg gctaagaaac aaggaaccac gctgggtgtc cttatccaga 1140
 aactaggaga tatccccgaa ccagtgatat atttttttta aacaattaga ccatgtcact 1200
 tcaggatgac ctgaatgcct cagggcagtt gcagcaactg ctcttttagg agatgaagtc 1260
 aataaaatgg ctttaggaca acatctggaa gttttaaccc cacatcaagt acaaggagtc 1320
 ctagaagcta aaggacacca gtagatgaca ggaggtactt attgaaatat caggccttgt 1380
 tgctaaacat tcctcatgca acccttaaga tacgccagac tttaaatcca gctacctatc 1440
 tgctgaacc cactggcacc ctgtatcatt ctcgatataca agtaatgcac caagtttatt 1500
 ccagctggct ggatttaaat gatgagctc tagataatcc tgaagtagaa tgttttatag 1560
 atagaagtag ctttgtgcgc cagggacaca gaaaagctgg gtatgctgtt gtcagtcaac 1620
 acaaggtaat taagtctcag gcctcaccaa cttctacctc agctcaaaag gcagaatgaa 1680
 tagctcttgc taatagccct gcaattatta atagctcata ttaatagccc tgcaattggg 1740
 aaatgactta gtaattaaca ttgtactga ttctatgtat gccattctgg tgcttcatgc 1800
 tcatggaagg aatggggaga atgaggactc ctaattgctg agggttcccc tgtgaaacat 1860
 cacttaaaca ttttaaactt attagatgct gttttgctga ccaaggaaat agctataatc 1920
 cattgcagag ggcattccaa aggagactct agtgtggcta agggaaactc ctttgcagat 1980
 gcaggagcta aggcagctgc attaaagcag ccagttggac ttgtaggcat gttagtggc 2040
 tctgccctgg taatgacaga accaagatat actaaagagg aataagaatg ggctaaagg 2100
 cagggtttta ttcaagatcc ttctggctga cttatcaatg acaacaaatt attgatacca 2160
 ggtgctaatac agtggaaaat agttaagcat ttgcatgact ctactcattt ggggaagat 2220
 tccttcttcc aattaatgtc tctctctctc ttttttttta ttttttgagc agagtttcac 2280
 tcttggtgcc caggctgtag tgcaatggca caatctcagc tcaccacaac ctccacctcc 2340

tgtgttcaag	tgatttctct	gcctcagcct	cctgagtagc	tgggattaca	ggcatgcgcc	2400
accacgtctg	gctaattttg	tatttttagt	agagacaggg	tttctctgtg	ttggtcaggc	2460
tgggtctcaa	ctcctcacct	caggtgatcc	atgcgcctca	gcctcccaaa	gtgctaggat	2520
tacaggcatg	aaccaccgct	cccagccaat	gtctcgtctt	tttataggaa	aaggcttact	2580
tacttagaac	agtaaagcag	gtaactcagt	cctgtgaact	ctgtgcccag	aataacccaa	2640
ataaccaacc	ttttccttct	ccttttagtaa	ggcctgttca	gcatagtggg	atgtatgcca	2700
gtgaagattg	actagtagat	tatgctcaga	tgtcccatg	taaaggattt	aaatatattat	2760
tagtattcat	caatccttta	ctgggtggac	tgaggctttt	cctacctggt	ctgaaaagac	2820
aaggtttcta	acctcctatg	aaaggcaata	attcctagat	ttaggctgtc	taatagcttg	2880
caaaacaata	atggccccat	tttcacagtg	acaattagcc	aaaacataac	ttcggcccta	2940
ggaattaagt	acctccttca	tttagtatgg	atgccaccat	cttcagaaaa	agtggaaaaga	3000
gctaatacaa	ctaaaaagta	ctatgccagg	aaacaccaga	aaccggacta	tctatatgtc	3060
ctgtagcctt	gttatgggtt	taagctgttc	ccaagagaaa	tctatagtgc	aacactttta	3120
aatgatgta	tggaaggcct	ttcttaacta	cagacttcct	gattgacata	gatactttca	3180
agtacaaaa	tatgtaatca	acttaggaca	aatgcaaaag	gtgctccttg	aatatggaaa	3240
tcaaagactc	ccttccccct	ctaaggaaga	gaatatgtgt	acaaccagc	caggagaccg	3300
ggtcctatta	aaaattggaa	ggaaggatcc	ccagcagatc	aactttcacc	caaaatgaaa	3360
gggatcctat	caagttctcc	ttagtaccct	aactgcagtt	aaattttctag	gaataaacag	3420
ctgggttcac	ttatctcgaa	tgaacacctg	ctcttataaa	gtcccacagg	ccaacaaaac	3480
acaaaagact	gatcccaact	attcctgtgg	gccaacccat	gacctccagc	tcctgttcaa	3540
aagaaacaaa	aggaatgggt	aacataaaga	tatggattgg	cattctattt	ttgggtataa	3600
gctggaatca	cacaaagagt	aacttatttg	ctaagtgggc	agactgtagc	ctctctacat	3660
aatccaacag	tttggtggac	tatgtagaga	attgccattt	tccttcactt	ccaggttgcc	3720
ctggcatatt	caaccagcaa	acctaagttt	atggggattt	tattatgatt	gggaaactga	3780
gcattataaa	tatagtccct	cttttctcat	gtaccatagc	cacacaggcc	ttaggccctt	3840
cctcacttat	ggagagacaa	gaaggcacct	ttttcatcta	attaggaac	agctaaatgg	3900
cacctcgact	ttaggttaca	ctgtacacaa	tagacttggg	tggatgacag	ttgttcaagc	3960
acaggtatca	ggcaaaacac	ctctatgttt	tgaagatgac	attaatagtc	accaccagac	4020
tgaaacccgc	aatatgggat	ggttgccacc	tcaacaatgt	aatcagaccc	ttcttttaac	4080
agaccaaagt	tgggtaggat	ggcaacacaa	tttgcaaaaa	atagatgcc	acccttcccc	4140
ttggggatgg	ttatgggctt	gtggaactca	tggctgggtg	tatttacttt	atagttggac	4200
ttgaaagtgt	tccttatctc	ctgggaacta	ccctcaacaa	attggactct	ctcctgtcta	4260
actgggatac	tgtaaaggct	cgccataggg	caacaaaaac	aggcttcttg	gtggttctat	4320
ctgatgctgt	attttcccca	caggcagcca	taatcaatat	caagttacaa	gttaaagcct	4380
tagccaagca	catggctgca	gctttcaata	atacacgcca	tgcccttacc	ctcctaactg	4440
aggaaacttc	tcagattagg	cagggtggcct	tacaaaacca	tgtgactttg	aacattttta	4500
tagcagtcga	agggggaacc	tgtgctttga	tcaaaactga	atgttgggct	aggcgcagtg	4560
gctcaggcct	gtaatccag	cactttggga	ggccatggta	ggcggatcac	ctgaggttgg	4620
actttgaggc	cagcctgacc	aacatagaga	aaccccatct	ctactaaaaa	cacaaaatta	4680
gccaggcgtg	atgggtgcat	cttgtaatcc	cagctactcg	ggaggctgag	gcaggagaat	4740
cgcttgaacc	caggaggcgg	agtttgtggt	gagccgagat	cacaccattg	cattacagcc	4800
tgggcaataa	gagtgaacct	ccgtctcaaa	caaacaatat	aacaaacaaa	acacaagtgt	4860
tgtgtgtatg	ctccagacta	ttcccataat	attaccgggg	ctatgaaagc	tctagatact	4920
catatctttg	ccactgatgc	actgccagtt	gacctatat	caacttggtt	ccaaccacta	4980
cccagttctt	ggaaaagcct	ccttttttagt	ttacttagga	tgattttact	tatttttgctt	5040
tgtgtgtgtg	gaatatatac	aattgtactc	tttatgtggg	aacgcaagac	aagcttactc	5100
aatactttct	taagttggat	acattaattt	tccagatttc	gccttttgct	gggactaatt	5160
tatgaacaac	cctcaccata	ccgaggcttt	ctgactgagt	tcctctctac	cttgaataaa	5220
agagactcta	ataattaggc	aggaatatca	tcgcccctgt	tcagcctaag	gaagttacaa	5280
aagactgatc	tttgtctatc	tgccaccctt	aggattaagg	gtcctcttat	aaagggaagt	5340
gggaaatatg	tcagagggtat	tcaaactaga	gtaactccac	cttaagtga	gggttaagaa	5400
aacataaggc	tgggacttgc	tgggctgcat	tcccagaaa	ttaggtattc	ctagcctcta	5460
gaagtttaca	gttaagggaa	cagattgata	acatgtacta	aacagaccca	gacttaggag	5520
tttcttggtg	tcccaatata	tagagaacag	aagcattcct	aattttgctt	taaagatact	5580
aatatcaatt	cttgcaaaat	atagtaatta	agaaaattaa	accttctctg	caaactcttg	5640
tagcagagcg	tatctcccct	tgatctattt	ttgtcttata	cataaacaag	cattgtacct	5700
aggggtgaaca	cgttcctcct	cttactttca	ggaacgtcct	actctgtcta	tggagtagct	5760

gttctttcac	cactttactc	tcttaacaaa	cttactttcg	ctttgcattg	ttgaccacc	5820
ctgaattctt	tctgttgaga	tccaagaacc	ctcatttagg	gtctaaattg	gggcaccctt	5880
ctggtaacat	ttttctggtg	accatgaagg	gaaaatactg	aggagacccc	caacccaaag	5940
gaaatagact	gcagtaccaa	ctagctgatt	gggtaagtgg	ttgggtacct	gggtaaagga	6000
tgggattggg	ttagaggccc	aacttagggg	agtttagagtc	cccccaacag	agagagttaa	6060
agaccctct	tgtaaaaggc	aaggacactt	gactgaacct	gggttccagg	cccaactttg	6120
gaaggttaga	gtccttccta	agatttatgg	gatttagagga	ccctttcagt	aaagttcctc	6180
ttggctaaga	atagggtttg	caccagggga	tgtaaactgc	tatgctgttt	gcattttatct	6240
gccttgtcct	ctttgctgca	tgcatacaat	ttttggctgc	tatctctgct	tactgtcat	6300
tttcaggaga	tttcatttaa	ttggtcttag	agattttaac	tttctgttcc	cctgtgtgtc	6360
tcttgattta	catccatttg	cttgtaaac	atcggaaga	aaaacattga	aggttccatc	6420
tctaaaattg	ctgatggaga	tttagcattt	aagcaataag	attacgtgga	tgtgactatg	6480
ttttgtttct	taataaactt	gcttttgctt	tgcatgtggg	acgtgctctg	aactctttct	6540
tgtgtgagat	ccgaaaaccc	tctcttgggt	ctggatccag	acttttttcc	ggtaaacattg	6600
gtcaggaaac	tgcagtcact	gtggtcattg	ctgtttcctg	ctgatggcct	ctcaaaactg	6660
tgatgtatca	tgtagcattc	ttccccctact	tccttcaccc	tgtgaccacc	acctcaaata	6720
ggcttgtgtc	ccacttcctg	ccataacacg	ttctatagga	gactgcgtgg	tacttgcaac	6780
ttcttggcaa	tttggtgtga	aaagcacaat	tttcacatct	acttgatcta	agatggagac	6840
ccagacaatg	tccatggagt	tggcctgagg	accaatgaca	aggaccatgt	ttccaaagcc	6900
tccataacat	ttaatccctg	caacacttca	gaaggctcct	tctgttatta	tcttcactta	6960
tagaagggga	aatgagggtg	agtgaagtaa	agaaacttgc	ccaagatcac	agtgcacagag	7020
ctggaattta	ctccaatgtc	agtgtgatcc	tttgaaacct	gtctttaacc	accatgtgaa	7080
taaaatcatc	tctttttattc	ttttttacatt	ccctgttcca	tattagcaag	agttaagtag	7140
ccagtacagc	aagctccaat	gttataggat	gaggactttg	tcttaggttt	atggcttggg	7200
tttattgaac	ccttgggtgc	cacttgtaaa	cattttccag	tgtcctctaa	cttgggggta	7260
gggagtgaag	actaccattt	atggagcttc	tcgaatagg	tgcatttttt	ttttcttttt	7320
ttgagacgga	gtctcactct	gtcaccacag	ctggagtgca	gtggcacgat	ctcggctcac	7380
tgcaagctct	gtctcccagg	ttcacaccat	tctcctgcct	cagcctcgct	agtagctggg	7440
actacagggg	cccaccacca	cgccagctaa	ttttttttgt	attttttagta	gagacggggg	7500
ttcaccatgt	tagccaggat	gggtcttgatc	tcttgacctc	gtgatccacc	cacctcggcc	7560
tcccaaagtg	ctgagattac	aggtgtgagc	caccacaccc	ggctgcattt	atttacttat	7620
gtatagttta	caaataattct	tctttctcat	ctcatttata	attaactaat	aaccttgga	7680
ttattaagag	attgttgttt	ttaacctatt	tagctgtgag	aaaggctcac	agaggttggt	7740
tcttgctact	taaaggttgt	tcccttattt	accagctac	ttgggacaat	ccagaacttg	7800
atctcaagta	ctggggctgc	cagcctcacc	ttcttgccctg	tgctagaggc	agttacccaa	7860
ggttcagaat	tcctgaatga	gtcctgaatc	agagacaagt	agatacctca	tgcatagcacc	7920
attgtccttc	cttttcagggt	ttggagtgtg	gtttctttta	gattattgag	gtctttcttc	7980
ctttgacatg	acaatttgtg	ttctgtcctg	aaaacctggg	gtgctgctgt	catcctgggg	8040
cagcactgaa	tacaaagtct	cccagagggc	aaacgctata	tgagggtcca	tcaaaattcc	8100
actaggaagg	atgcaaaacta	atgcagtcaa	atcttagaag	cattgtgttt	ggtatattgc	8160
tataaaggat	tgaacaacaa	ttaaacttag	tgctagttag	ttatatttga	aggttagaac	8220
attgggtcca	aatttcaatc	agaagtcttc	acaagtgaag	tattcagcca	ctcacttttt	8280
atggttctgt	tatgacacaa	actacttgag	ttttgaaaaa	caaaatattt	tagccaccat	8340
tttattgaca	gcttcattaa	attgtcaaca	attatatgaa	aaattattta	gcaaaagcaa	8400
acaaatgcga	tcccttggtta	agataactac	aagaatttaa	ttttttttta	atgaaaacaa	8460
gtttattaa	aaagtaaagc	aataaagagt	ggctattcca	taggcaaagc	agcagcctga	8520
gctgctgggt	ggccattttt	atggttattt	cttgattata	tgctaaacaa	gggggtggact	8580
attcatgagt	tttctaggaa	aggggtgggc	aatttcttag	aactgagggt	tcctctcttt	8640
tttagaccat	acagggtaac	ttcctgatgt	tgccatgaca	cttgtaaact	gtcatggggc	8700
tggtaaagag	gtcttttagc	atgctaatat	attataatta	gtgtataatg	acgagtgaga	8760
acgacagagg	tactctcggt	ctccatcttg	gctttgggtg	gttttagctg	gcttctttac	8820
tgtaacctgt	tttatcagca	aggtctttat	gacctgtatc	ttgtgccaat	ctcctatctc	8880
atcctgtgac	ttogaatgcc	taacctactg	ggaatgcagc	ccagcccagt	aaacctcagc	8940
cccattttgc	ctagccccta	ttcaagatgg	agttgctctg	gttaaaacgt	ctctgccata	9000
tttccccct	ccatattttt	aaggaggtaa	atgtgagtag	caaggtagta	aggaacttct	9060
tgtaaaaatg	gcaatatgta	tcagtgattc	tcccatcagg	ggcaagacca	tagtttggtg	9120
aggcacattc	tttactaggt	gagagccaag	gggagtgaca	gcaatcacca	catgaaatta	9180

ggcataatcc	atagttttatc	tgtatagcag	attgaaaacc	cagaaaaaaa	ttgagaaata	9240
aattattgatg	taaatacatca	gattttttcag	caaataatagt	ccttggtttcc	cccaaaaata	9300
aacaacacatt	ttatatTTTT	aaatatTTTta	TTTTcctggt	cTTTgtgaaa	acatacaata	9360
atatcgaaac	ctctctgctc	taacacagag	ggaaacactg	cataattaac	attaaacaag	9420
gcagtatgcc	ttacaagaaa	gacataaaat	gtccaagggg	tatttagaac	atttttagttc	9480
ttaaagcttc	aacatgagaa	atgttgacca	cacactgtga	aatcatttca	ataaataaca	9540
actgacattc	atctttacag	ttacaaaata	gacacacata	catttccctg	ccgtcacatt	9600
gatctcactg	gccattttct	tggattcctc	agcctctatc	acagtggctg	acatgtgata	9660
tgtcatcacg	aagaaatatt	aacaaatgac	tagagaatat	ctgcaaacct	tctatcttca	9720
aattaaatat	gaatcaggat	tgaactaact	tgggtttgac	ctaaaataaa	caataaatat	9780
aatgggagag	tgtgcaagta	gattcaatca	taaccttatt	ttacacataa	aatattaaca	9840
tagaatcttc	taaaacaaaac	aaataaataa	ataaataaat	aaatagaaga	cttctcctaa	9900
gtgatgctca	aacacattag	gcgcaatcca	ggtggcctct	gcagctgtgt	ctctctttcc	9960
tcttctgttc	ctgtaagggc	agggcctcct	tcaggaacag	ccaccaataa	gcttctcctc	10020
tccttctggt	cagttggatt	tgccactgta	atgagaaaaat	gggtgccctg	agtaggtgct	10080
caggaaagct	gactgcacaa	cagtcttctc	ctgtcctggt	tccccaggct	ctagagtttt	10140
ctgagtcag	tttccccagc	ctggcaccca	agtgggtact	gcctgtgaca	gctgtgctgt	10200
gtggcaagga	cctctaggct	tgggatgctc	ttttaggaat	gggggtgacg	tgggggtggag	10260
gagtggcagt	ctacactgtt	ttactggcta	aaacagccag	agcctattgc	tctttgtcat	10320
actgggcctc	acttgagcct	caaagcaacc	tcatgatgta	gctaccatta	ttttccctgt	10380
tttgctgagt	ctcagataaa	ctaaataata	ttgtctctga	gtgacatggc	taataggtgg	10440
tggcaaccag	ttatataccc	agtgcataat	tattgtgaaa	tctctgcaat	tcaaccctaa	10500
actttttaca	aaaaccaggg	ggtctgcttt	tcaggtctga	aagtcagtag	gaactagggg	10560
aaatgaagct	tgtgtttttt	aacaggtgga	aaacacttca	gcacaactgg	caaactccaa	10620
tgagacctta	catgaaagca	gttttaccta	cattcactgg	caggagggaa	gaacctgggt	10680
ggtgaccctt	gggactggg	aatatcctct	ggcaccagaa	cagattaata	accttaatgg	10740
caactttaat	tgtgaaaata	ataatTTTT	cagtcctgca	gctaaccctg	ggttttctct	10800
atttactttt	tagggggcag	acgccagtat	ttctgaccaa	cagctccagt	cgctgtgta	10860
catggaat	acaactcact	tttccagcat	ctttctgatg	attttcttaa	cccatgggag	10920
atgcgggggt	gagacaagct	ttctgcccac	tcttgagtgt	ggctctgcag	agagaaggga	10980
atctcgtgag	acaggaggtc	gggctgagga	caggggtttg	ggcagcggga	gagtcgggga	11040
ccccagcagt	ggcagcggca	gcgatgggag	agacttacat	gacttcgggt	tgggcgcagt	11100
gggggtccgg	ggacttcacc	ttcacacttt	ggatgttctt	gaggtgaatt	ccctgcaggg	11160
tctgcaagca	ctggcagcgc	agttcagtg	ccaggggcgc	tcctagggaa	gaagagactc	11220
gctgattgag	cggggctgtc	ggcgcggggc	gcccacccca	gccgcgtccg	gcccggggac	11280
cccagggcgc	cgggaccac	ctgctgcgcg	ccggctggcg	gccaccagga	gcaggagcag	11340
cagcgccacc	cgcaggagcc	ggggattgct	gggggcggcg	gagagcgtgg	cgcgggccat	11400
ggggctcagc	aggcggttcg	agcggctgtg	cgaggaggag	agctggcaag	gagctgcctg	11460
tggcccgggc	tctgtggctc	tccgagaacg	gcgaaccctt	tttatgcatg	gttggggctg	11520
gaaagcccgg	agtcccgggc	cagggaaatt	cccggagctc	cagatcgatc	ccgagttcgg	11580
aagggaaggc	atggccccgc	ctctgggggtg	gaggggggtc	ggggcactca	cgagtgcagt	11640
ccgggtctga	ctgtcttgcg	taactccccg	caactgtggg	atgttctctt	tctgccccga	11700
atccctggag	cgggagcgag	agcccgcgcg	tctcagagat	accgagataa	ccgcctgcga	11760
ggaggcgctt	cgtgaaccac	gtgcagtgcg	tcgtgggtca	gatcccttag	acccacgtag	11820
ggaccgcgct	acatccttac	cggggggagt	tacttctctg	gaagacattt	cagttgttgg	11880
gattgaaagt	tagggcaaga	actgcagcat	gtcttatcta	tcctctctct	ttagtttggg	11940
ttctgcaaat	ttcattaatg	tttgaaataa	acgcacgctt	taacagtaca	tgtgtcatct	12000
cagatgacgc	ataagagctt	ttgtctcctt	cctggtgttt	tatgatctta	aaagcaaata	12060
tcacgtgtgt	gtgtgtgtgt	gtgtgtgtgt	gtgtgtgtgt	gtgtgtgtgt	gtgtgtttca	12120
acgtagtggg	gccaggtgtt	gggtgcggga	acagaccatt	gcccagggtt	caattcagtg	12180
tttatTTTT	ttaacagtgt	tgcaatcccc	catcctttct	ctctttgaaa	tcttggaaca	12240
tctcgaaact	tagtaattcc	agtagcatca	atTTTTtgtt	gtatggaagt	ctgtgttttg	12300
atccatggaa	gtcactggga	gctgcgaggg	gcctgttggg	ctcaggaggt	ctgccttttc	12360
tagtgctgtc	cctgggcaga	aaaggccata	gacaccacca	gaaaaggagc	agggaatgag	12420
actccgcttg	tttactactc	taagcacaag	cagacatgtc	tgatatatac	atactagatt	12480
gctaacataa	ttgcatttcc	atgccatatg	tatttaccag	catcctggga	ttggttccct	12540
ctagagaaac	agctatcgag	gaaatTTTT	ttctagagga	atgtcaataa	agcatttcca	12600

agcctgttta	gctgatgcct	tctcactgga	ttactgactt	ttcatcatca	atttcaatga	12660
ccccctctct	ttaaaaatta	agctgtaggc	ctacaatact	ctgtctttaat	tcttcctggg	12720
ggatgcagac	ttcagggata	tggagatatt	ctgccactgc	tatgagaagg	gctgggagtg	12780
gcacgaggat	gaagaagtgg	gactacctta	ggaatagagt	gttccttggg	tgctgcagct	12840
gtagagatca	cttgataagg	atgtcagggc	tgaagtttca	gccataccac	taacttgctt	12900
catgaccctt	ggtaatttat	gctttatttg	ctcatgtttc	tcccctgtag	aagagcttat	12960
aatagtgcct	gcctcacggg	gttgtagaa	gtattgattg	ttaatatgtg	taaaccatca	13020
gtgcatgtaa	agtgttatgt	aaatatgtgt	taaataacaa	aatagaagtg	gtgtttcaca	13080
accttactga	tataggctgg	atgtttgtgt	ctctttcaaa	ttcagatgat	gaagccctga	13140
ctcccttatg	tgctaataatt	agaagacagg	accatgggaa	gtaattaggt	ttaggtgagg	13200
ttatgaagg	atggcccca	tgatgggata	agtgccatta	cagcaagaga	tcagtgaagt	13260
ttcgatctct	ggctctctct	ccctttctgc	attgtgagga	cacagcaaga	aggccaccat	13320
ctgcaaaactg	agaagagggc	cctcaccaag	catgaaatct	gccaggatct	taatcttggg	13380
ctccccagcc	tccagaactg	tgaataaatt	gttgtttaag	ccccctagcc	tatggcattc	13440
tggttatgca	gctcaaaactg	actaagacac	ttaactaaac	agaagcactc	tgataaagcc	13500
ttatgaacac	acacacgcac	aaagaaagaa	atattttcaa	agaaacatct	tctaattttac	13560
ctttaaaatt	tttcagcatc	agaaatttta	aaggagggtg	catttctatc	cttatgggat	13620
cttacaataa	ttttttgatc	cattgtttgt	ttgaaatttt	agtttcaatc	actttccaca	13680
taaaatgaga	ataagagtaa	aattctaccc	tatccattta	ttagaaaaga	tttatgaaat	13740
gactctgcct	tgggcattaa	cagctagctg	cccaaacttc	tttattttgt	gctaaagaac	13800
taaagaacaa	tagaaaacat	cagcttataa	tgattgccag	actcatccca	aagtattgat	13860
gtgagtaaat	agaaagagta	aaatttctat	tatctacagt	aacagtcctc	caaaaagatg	13920
agaaatttca	agaatcagcc	catcatttgt	aaaattatgt	acgttattcc	tagaatttgt	13980
ttactaaaaa	ttatttgctt	taggaaggga	agtagaattc	ctttttcttt	tcttaataata	14040
ccactttcca	tgatttaact	tatgacagcc	ccagaccaag	cttctgaagt	ttttaagggt	14100
accagtgtta	tgaactttac	cataataaat	tccttcttgt	cttaatatga	gttgagtggc	14160
actgttacag	gcacaagttg	taaacccatg	caattactaa	ctcaaagatg	ctatctctaa	14220
aatggaagta	cagtttccta	aattccattc	tcccctttaa	tttttattgt	atttttcaga	14280
tttgactagt	acaatctaatt	atacctgcaa	aatgtaggct	tgctgctcca	tgccgaccac	14340
tgacattctt	tttacttggg	cagcaaaaatg	agtgggtggg	ctctgcttta	ccgtgaattg	14400
ccttgaagac	tttgctgata	taacctccaa	catatagctt	gctcctctag	aggaacagac	14460
tagaaaataa	ataaagaagt	acaactgatt	ttagagatag	atctgatgga	ggttgagata	14520
tggggctctg	gaattacaga	atagaagaca	gataacatgg	ttcatgataa	gacttgtag	14580
tcctcacact	gtttatgctt	agtgactcct	ttgctttcag	gttttgctgc	cacgcataca	14640
aagtggacag	tggtacaacc	cctttgttgt	gtctgactgc	atgaagaaat	acataattga	14700
cttagttaca	tactatgtgt	atttcttgtt	atttttttca	ctaaagaatt	aaggcagctc	14760
ctcaatgacc	agagcctagg	aatacttcct	agtattataa	acattgcaat	tgacatgttc	14820
tgtggggctt	ttgtgatttt	ttgaaaactg	tggtttatat	tcattgtgct	aaagttttcc	14880
ttactggctc	tggcaccctg	gctttgggtt	gtggctcctgc	ggaagaaaca	ttcttccttg	14940
tctgtgggtc	tttagtggtt	tgcttgtag	ctcagggtt	gtggccacca	ctcatcgaaa	15000
catgtgctct	ggagataaag	cgccaaagga	aaagaaggga	agtaataatt	atttattaga	15060
ttccaattct	tgattagatg	cagtgcctga	gtttttcagt	gtactgtcat	tttaataatt	15120
tcaagaatgc	tgggaggtg	gtatcatgag	tcttatttta	taggtaagga	aactggagta	15180
caaggctcta	gaagtggaat	taaaattcaa	cccaagactg	tctgactcag	aagctcatag	15240
ccagtctttc	tctagacaag	aaaggaagtg	acaggagaag	aagaggacat	gtaaaagaat	15300
cttaattaag	tctatggagg	atattttatt	atttttcaac	cctaccagaa	aacaatgcat	15360
ttattaaaaa	atttaataca	gttttgatta	ggaaccaaac	agacatgtag	aagtgatgac	15420
aactagtagc	ctccagagtc	ccagcagccc	agagaatctc	ctgcttattg	tgccgtcagc	15480
ccccaaattc	attccatgaa	gttcccagca	actcccacaa	ccatatcaga	atctgatatt	15540
atgattgaag	gcaggctggg	agtgggtgct	cacacctgta	attccagcac	tctgggaagc	15600
caagacagta	ggatcacttg	aggccaggag	ttcaaaacca	gcctgagcaa	gatagtgaga	15660
ccctgtcttt	atggaaaaaa	aaaaattgaa	ggcagatggt	agcgtaggta	aaggatctag	15720
ctaagcatct	tacctctagc	agctcttaaa	gtatcttaga	aggcactaat	aagaaggtag	15780
ataccactat	aaactgttaa	aggttggtct	gtcatcaaga	gactagagca	atatttcaat	15840
atgtataaac	tacaagtcac	gatccactgg	agggtcataa	agtcagtttt	gtgggttgta	15900
accagtattt	aaaaatataa	aggggcagtg	gctcatgcct	gtaatcccag	aactttggga	15960
ggccaaggcg	ggcagatcac	gagaccaaga	gattgagacc	atcctggcca	acatggtaaa	16020

accctgtctc	tactaaaaat	acaaaaaaa	aaattagccg	ggcatagtgg	caggtgcctg	16080
tagtcccagc	tacttgggag	gctgaggcag	gagaatagct	tgaacctggg	aggaagaggt	16140
tgagtgagc	tgagattgca	cctctgcact	ccagcctggc	aacagagcga	gactccacct	16200
aaaaaaaaata	taattgtata	tatacataca	catatatata	tgaataaaaat	aggatagaat	16260
tttaaaatgc	atgtgccata	atgcatcaca	tattgttagt	ttaactgtta	ttttatgaca	16320
cttttgtgtc	ttatatagat	aggtaactgt	gtaaaactaa	acatttgatg	cacaagatgc	16380
aaaaacagaa	ctcccaggag	tgaaaaatc	ccttcagaga	cgttattata	ttgatcaagg	16440
ctgtgactat	ataataagtt	cccagtttgt	agacattatc	tcctgagaat	ttccaatcag	16500
gaaaaaaaaag	ttgaagcata	ttccatttta	atgtcatcac	tcctaaaaag	tttgacacaac	16560
agggagttcc	agtaaatgtc	tgagcttttc	ccagcaggaa	tgccaggttc	ggatgttctt	16620
gctgataagg	gtggccactt	ggcagtggtc	tcagcagagt	tgaaagatta	acatagtacc	16680
agtattgggt	cgcttagcag	aatttggttc	agtcccttgg	tcatttgggc	cacaccgacg	16740
aattattata	tccagctatg	aatgttgctt	gtggcaggta	caaaagggaa	ataaagaaaa	16800
tattaaacct	taatacttta	ccattgtcac	cctacttctt	ggtgtgttaa	tttttcaaaa	16860
aaaatcagtg	gaagtacctg	ttcaatttta	acattctttg	tttatttttg	ccaaaatctt	16920
tgtcttttct	aagtgtctaa	ctcaacctac	caaattatct	atgacagtac	acaaataaca	16980
ataactaact	aatgaaaatta	taattatgaa	taataactaa	taataacaaa	aatgtctctt	17040
tgtacttttt	atatctggaa	gagggctgag	attttgcatt	catgtgcata	tgtgtgtgca	17100
tgtgtgtgtg	tgtgtatgtg	tataatatct	ccttacatgt	agacacaaaac	tcaagagata	17160
gatactcaaa	atatgcccat	ttttcacatt	atgaaaccaa	ggtatctgcc	atactaacaa	17220
aattggaact	caaaatatgg	gtgaaagaga	aactttgaat	gtttatacgt	atgtgagtga	17280
catggttgta	tttgtatttt	agcaaaataa	cttttgtggc	attgaaggta	aaatgcaggg	17340
gaaatattta	ggttacctgg	gatcattttg	atattttcca	aaattgtttc	taagatttat	17400
tattgtgggt	ccacaatacc	ccttagtttt	ggattaattt	gacccacaga	aggtattgag	17460
gcaatacctt	tctgaaaact	ccatatttga	gcctgaagca	tgctttgact	ttttcaagac	17520
caatatgaat	tttatatgct	aacaatgtaa	ccacattctt	tgtttctatt	atagaatttt	17580
attgaattta	atacatatat	tattaattta	taatacataa	attatttgtt	ggatacaaat	17640
tgaaagtctt	tggactacag	aggagtctt	gtaataatat	atttatctgg	gatgtaatcc	17700
ttttctgtta	catctttact	gtcatttttt	tctctacttt	gcgtgcatat	ccatgataaa	17760
aataggtaga	aaatacagtt	ttgtgagata	aaactattgt	agctctcttg	tatacttgca	17820
acaattacac	ttggaacaaa	acaataacgg	tggctatatt	ttaaatttta	aggtcccaac	17880
agtcccgat	aaaagtctaa	tctctacggg	ccttaaaact	atttccttta	aatcagatta	17940
aatttgacta	tatgccttca	ttccaccaag	gagaaaacta	ttcaatctca	gtcattattg	18000
tagctcccag	accacactga	aagtacaaaa	gggtcccaagg	gatttatcca	agcaaaatat	18060
tcagggctgt	ccatctgtac	tttgacttat	acttgttttc	cataaaagga	caaacattga	18120
tatggtcatt	ttaaagtgcag	cactgtccag	ctcttatcca	ttctgtagca	cagaaatctt	18180
tgctaagggt	ggtaataaca	gtgcttggtg	atctcttaag	tacaaagtac	agtctttctt	18240
ccagagtcct	gccacctccc	tggaaggaga	gagcagcaag	gagaaacaaa	actgttaatt	18300
ttggcagtg	gtgaaacact	gtgatggccc	cttttccctt	cccactcctc	cctccctgtg	18360
gcacacagcc	aggaagcaga	tgaaggatag	ttcgtgagtt	caaaaagaag	gggagatttg	18420
agagtggtaa	gaaaaataaa	ataatgaatg	attctcaaga	gagggaaaag	agaggcacat	18480
ccaagggatt	tgaggttact	tagctaactt	tgaagatttt	gccaaactgg	agtccaagat	18540
tcaggaatga	ggattttgaa	atgagaaata	aagttaaagt	agctgaaaag	gtggaattga	18600
gactaggagc	tacttctgtg	ctccagtgcc	cttctgggtc	tatatcttct	tcttgccctta	18660
ttcagatggt	tgccaaacta	acattcaggc	catgtaggac	attgactaca	ctgtctctcc	18720
tcttccctcag	tgcagttcta	aggctacaca	tatactcaac	cactggactt	atttattaaa	18780
cagcaaccat	atttccagga	ttgagggagc	cactgagatc	cagaaatcaa	agtgtctatt	18840
ccttccctca	caagagccac	actctgggtg	agcagacagg	gatgtcaaca	ggtggtaata	18900
accagtggtt	tatgctaggc	attgtgtatg	attacatatg	taaggaaactg	gggataaaaa	18960
gaagggcaaa	atactgaatt	tgtccttaaa	gtgcttaaat	tctaaaatgt	agaataaaca	19020
atttttttta	aaaaatgtat	tatgttatgg	tcagttccat	atgggggtcca	ttactgctct	19080
tagactcagg	aaagaaggtc	cccctgtcct	gagcctaagc	ttcagaagat	ctcactagca	19140
caaccttgca	aaaaaaccac	aatgtatta	gagaaccccg	gggggcactt	ctgccacctg	19200
aggaaccaga	gcctagagtg	ggcgccaaat	gacccttaac	ctcctaaact	tccttaacac	19260
tagatactta	ctttcttgat	taacgaagtt	caagcccaag	gctgagatcc	cagagggaca	19320
cagtggggag	cctaaagaat	aatgatcatg	gtgggtgagc	tccttctgt	tctctttggc	19380
tctggaatga	ctatgaggag	ctcaaagcat	atttacaac	caaaattttc	acaggaact	19440

tggccgaaga	agcttggaaa	aagtcaagag	gaccatgtat	ccttactgcc	gactatttcc	19500
acattttcca	catctttttc	tgagatcagt	taataagcat	aaccctaagg	aatcagtcga	19560
ccagatgctt	tttaatttat	tctgaaagct	cagtgtctag	gtaacttacc	acagctgaca	19620
tattacaatg	tgtgaatata	gcatcaaag	tatgctttgt	ttctgcatcc	aagtagtgct	19680
ttaggaatct	tattgtcatt	gcattagaag	agtaaaatgt	ctccaaatct	aaattaatta	19740
taaaataatg	taagaaatga	ttgaagcatc	atctaaaatg	gcactattgt	ctatagaaca	19800
aaaattatgt	gaccattttca	attataaaaa	tgtaattact	aattttgctg	aagtgaagaa	19860
aaataaattt	tatataataa	atatagaata	atagaataaa	tcttaaatta	tgcatgattt	19920
tattttgtat	gcatccagac	attgcctaca	caataacaga	ataccagat	atggaattac	19980
aaattcactt	ttctctgata	ttttgctgat	tctcatcata	caaattccat	aactttatat	20040
atttttaaaa	tgttattaat	atatggctcat	gtgtcacatg	aagatcagaa	cgcatctgcg	20100
aaaatctggc	attaggctgt	ttcctccttg	tgtgaacatc	ttagagtcca	cttatgcaaa	20160
cccagatggg	gtagcctact	ccacacctat	gctatatgct	ctattctatt	ctcccaggct	20220
acaaggctgt	acatcatggt	gctgtactga	atacttaggc	aattgtaaca	caacagtatt	20280
tgtgtatcta	aacacacaaa	ggatacagta	aatatatata	ttaatagtac	tgtaatccta	20340
tgctctcacc	attgtgtatt	ccaactgtag	ttgtccaaaa	tgctcattatg	tagtgcata	20400
ctgtatatct	gtgaagacag	gaagatcctc	agactcattt	tatttaacat	tttgtttagct	20460
agttaagaaa	accgtaaata	tttagacaga	gaatcatggg	cttctctgaa	ctctctctca	20520
agacccca	attgtagat	atggcctcat	gaagcattga	agagtgcata	tgaggagaaa	20580
ttatgaaaaa	ttatcctaga	acagatgact	gaaaagatga	attttgga	aaatctagg	20640
tattataaca	tattttaatt	tgtactaatt	ttgacacccc	ctcagaggaa	tttttatggt	20700
tttgaaacaa	gaattatttc	tgtttttatc	tacacacaga	gttcatttta	taagtgttg	20760
gaacccaaca	gagcttaatg	aattgaatag	gatgttcttg	ggaaagagag	tatagataat	20820
acgcttcaat	agttaagaca	tcaggtgaga	aagccattaa	ttttagttaa	aattaccatt	20880
ttaattagtc	attttatgat	aacatagaca	atggaagatg	attaagaaaa	atgaagaatc	20940
agcatttctt	gattcttcaa	tagacacttg	aaaaactaca	acacaaggaa	aaccactgt	21000
ttgatggctt	aagatcctat	cccactatgc	tgacatttgt	caaaacactt	aaattgtttg	21060
gtttaaagaa	actccttttt	atccctgcta	ctaatacaaa	gaatataact	gtgtttgttc	21120
attgaagagt	ttctaagtat	tagaatttca	gcaacaggaa	attcatttct	caacttgtat	21180
tcttcacaca	aaaggcatca	aattgctcat	gagttaatag	gttgacagct	attgtcattt	21240
cctgggtggga	aactttcata	gttagaggaa	aagaaggctg	aacaccagat	gctgttcac	21300
atgtattttg	ggatatgttc	ttgaaggctc	gagatttaca	ctgaatttat	aaagcaatgc	21360
cattgagtca	agtagagaag	aatctagatt	atagaacaag	gctgtgaagt	cagatgggtg	21420
tgccaacagt	gtctgctgtg	cagaaccttt	agctcccact	tctctctcac	atgcactgag	21480
tcagaaaatg	ctattttgta	ggctgtagct	acttgtcagg	tttatgactc	aacaaactga	21540
aatattagcc	aaatgaaata	ttgttggtga	attcagggtg	ctcactcata	gcacatacag	21600
tggtgaatat	aatcatctat	agcttcaaat	gtgctggcca	tgagtccact	aagaaatgca	21660
gaaaagaagc	aagaggagaa	acagctctgac	cttagctgca	aagggcacca	ggatgccagc	21720
atgctagagt	catgctgggt	tcccccttca	tggaagtgc	aggcccatga	caaatttacg	21780
caaataatgac	atggaaaata	atttcttgaa	gaaaacttct	tttgccatat	gtttcctggg	21840
tttcttctgg	tttggcctgt	gaatgggtatc	agtttatatt	cgagtctagt	atccaatatt	21900
cctgggaagct	agggctgagg	aatgttcatt	tcacaggatg	gccaaggctc	gatatgcaag	21960
gctgggattg	agtgaggccc	cagggcaggg	tgagaacagg	aagcggtttc	actgacattc	22020
catcctttc	tctccctgac	cactcccatc	tcagagtggc	caaggatcac	tgaagaaata	22080
gtaattgtca	tctaaacctc	ataacagggg	tgtctggcac	ttgagagttg	accactttca	22140
atttattcaa	gctcccatc	aaaaaaactc	tccttgactt	acaggatatg	aataccaatt	22200
ccctaaagca	aagcatagt	agaatttcag	taaaagaaaa	gaaacgaaaa	ccccagaaaa	22260
agtattcagt	aattgaagag	tcaccatccc	gagggctcta	taggagctca	cccttggtcg	22320
gtgagaacta	ctcagtcagc	ctcacttacc	tcattgtctc	ggccagctca	tacaggctta	22380
caagagcagg	ttattaaatg	gtcaggaatt	ttgatagcca	gttattcatt	gttggaagca	22440
taaatttgac	cacagtggga	gtgtttatgg	aaatcagcaa	atgctacaaa	tctgattttt	22500
ttttaaattt	gaaagctggt	ttaccaacac	accgcggtt	atagctctgc	ataaacataa	22560
tctgtatcaa	ctttatcctc	tttttcctcc	ccttactata	gcctctgtcc	tctgccctca	22620
ttatcctctg	ctgggatctc	ttgaatattt	tttccccctt	agctggtttt	ctcttttact	22680
cattgatttg	tcctgggttt	catcatctag	gcaactctca	cgcacagaaa	attcttgagg	22740
gttggtctca	ctagactgat	agcaatacca	cttttattta	ttattattat	tattattatt	22800
attttgaaac	aagcaaaggc	tctaggaatg	aaatactaga	agatgaagga	tttttttctt	22860

ctggatcata	aatctgggca	tcccatgcct	acatgttctg	ggactcatga	ggcattctat	22920
tgatccccc	attgctatta	atagatacca	agtgaaaatt	tggtatctct	tcccatcagc	22980
cctaattctca	gaatgcatta	tcttttctaa	gcaacaactg	aagcctgtgt	gcactagcag	23040
ttaaagtgtgt	atctgcagga	ggtttaaata	ttcctaagtg	aatgtgggaa	gtggtagtgt	23100
attttggaat	tcaagggatc	ttagaaataa	tgtagtctaa	tttgctcatt	agtctggtga	23160
gtaaacagag	tttcagacag	attagcagtt	agtggtagaa	tcagtactag	aattcagatc	23220
cctggcttcc	tcttctgggc	attttcaa	ctgcaacaat	gtctatctta	attaacatta	23280
taattaggac	caagataatc	ttcattcaac	tcaacaaata	ttttttgact	accagatata	23340
tttctatgtg	cacttatttt	atactaggta	ctgttccagg	agttgagact	accaagaagt	23400
tctctacttt	ttagagcatt	cttttgagaa	ctaacattat	ttgtattagt	atgacttaac	23460
tctttgttcc	aggaaattct	tacatagaaa	ataaaaactaa	gctcatggag	aactttgcc	23520
tttgcttgag	gaaattcttc	taagtcagtt	tattcaggac	atcagtttgc	acatctgagc	23580
cagcatgatca	ctcctcagac	aagttcgctt	tttctagcaa	gaccctcacc	tgttttgtcc	23640
actaactcta	ttatgtcaac	aactgtgccc	aattccagtc	cattccctac	cttgtcagat	23700
cagttttaaa	cattttgagt	ccaattctct	gaacatcctc	cttctgagac	actaaaatgc	23760
tgtcagagca	ttgttctctc	tggtgagtaa	ttctaataaa	tttaacgttt	cctgattgaa	23820
gggggttttt	gttgttgttg	ttggtagtat	ttctgatgaa	ttggcagttg	atatgttcta	23880
ttggagacta	gaacataaga	atggggaagg	tgatacttat	aataatctat	ctgggtatag	23940
ttaggatctt	cacatgccac	actatgtagt	gacataattt	gacctggaaa	tagctggtca	24000
cattggctat	attgatagca	acaggagata	gacaaattct	taggcagaca	ggggatgcgt	24060
ccctggtaaa	acctgatctc	caagccaaag	acagcctgaa	gactgaaaac	tgagctgcca	24120
gttcggggta	gagcccatga	ccagagttag	aatttcctcg	atgcctttta	gccaatataa	24180
tgatgctttt	tccaggccca	cccattggacc	aatcagcata	cactccccc	ttctgaacc	24240
ataaaaaacc	caaactcagc	cttacagaca	gccacctgct	tttgggcctc	ctctcacaca	24300
gaggaccatc	cacttcaagt	cccctcttgt	gttgagagct	tttctgccac	tcaggaaaat	24360
tcttctctgc	tttgctcact	ctccgggtgc	tgtgtacgtc	attcttcttg	gtcacaggac	24420
aagaaccctg	aacatgcca	aagggtgtaa	cacatactcc	tgctcactga	gttacaggag	24480
tgaaaaaaac	cactgggtgc	cgcattgccc	tatttagcag	gtacaaatga	gctgtaacac	24540
aacacacccc	cactctccaa	gctgcaggca	gcaggagag	ctgtaacatg	cctccatcct	24600
ccgagctgca	ggctcaaaga	agtgaagcag	ttaggcacta	ttccctcctg	gccagcttgc	24660
tgaactacaa	aagctgcaac	atcttctggg	agcttagacc	tcaggattcc	ccaggcgaga	24720
gctgtaacat	cacctggggc	tccacagttg	ctggcatctc	tgagttttca	ggtgccactg	24780
cattcccttc	atctagactc	cggctcccaa	tgcaaaagct	gcctgtggca	tgccaagtgt	24840
agccacaggc	aaaacacaga	gtccctgttc	agatgtggga	tccaagcagg	tagcacaagc	24900
tgagtacagc	ccatcaggct	gagtgggaag	agtgaagcca	gcaggccttg	gcaagactac	24960
aggcagaggt	cacagcagcc	acagagattt	ccagctggtg	aagcagcact	gaaggagtcc	25020
tgtaacagta	tgttagtcta	caaacttggt	aaattctcat	tctctgtttt	ctgtgacatt	25080
ttgattttta	aaattttatt	ctccaataca	tcgcaaggac	tggatatect	gccctctatt	25140
ttgaaagtat	ggtgtccaaa	ttcataggag	aaggcaaggg	taggtgactc	agaaggcaca	25200
cacacaaaaa	agagtcattg	gaggaacaac	ccaggaagcc	atagaagaat	gttatcccaa	25260
actagatgga	aaagttttgt	ttttatgtaa	tttagaaaaa	cattcttatt	atttatttgc	25320
ttaaagtttg	tcaccatttt	ttcaaatttt	ttttatagaa	tgccatccta	tttaaaactac	25380
tatccacaac	atgaaatata	gttaccacaa	acataaaaaa	agccaagtgg	tggaatgggg	25440
aggaggggacc	ctgaactggt	gaccaggagg	tggcctctgg	taagcctcac	cataccttga	25500
tgaaagagcc	ctcaaaactc	tccatctcct	ttgactttta	ttctgtacaa	tcttctaatt	25560
tagatactga	tatagtttgg	atgtttgtcc	actccaaatc	tcattgtggaa	atgtgattcc	25620
caatgtttgga	ggtgggggtct	ggtggggagg	gaatggatct	tggggacaga	ttccttatga	25680
atcgcttagc	accattcccc	ttggtgataa	gtgagttctt	gctcagttag	ctcatgtgag	25740
atctggttgt	agagtctggg	accttccctc	ttctctcttt	tgatctctct	ctcaccatgt	25800
gacaatcact	gctctccctt	tttcttttgc	cgtgattgta	agtttccctga	ggcctcacc	25860
agaagcagtt	gctgaagtca	tgcttgcata	gcctgcagaa	ccatgagcca	attaaacctc	25920
tttcttttat	aagttaccca	gtcatgggta	ttcctttata	gtgctttata	gtcctttata	25980
gtgactcata	aatggcccaa	tacaggtact	tagccttttg	gttaaaagat	accaacacat	26040
agggtgactag	attgcagatc	attggcattt	tgaattgttt	tttaagtacc	catattactg	26100
tggtttacgc	caaattgaat	ctattatgta	gaaatatgcc	tataaaacta	ctttcaaatt	26160
tgtacaaata	tcagtttctc	aaagcgtata	tatatatata	tatgcatgca	tgtgtatgtg	26220
tctgttttaa	atacacctgc	tggggattag	cattgagctg	aaagacaagg	tcctgccctt	26280

gccctagaag	agtttgcagt	gtagatggag	accacctgac	acctcacctg	atccctgata	26340
gcaattccag	gccaactttc	ctaagcacta	tgggaattca	gactaagggc	cagatcaccg	26400
ttgcctgaga	ttccattgtg	atgttagaat	tcacattctc	attcttattc	aatagaactg	26460
actcgttcac	cagagcacct	actatgttcc	aggtggtatc	ataagaactt	gggagacatc	26520
actaaacaaa	atagaaaaat	ccctgccctt	atggagctga	cattctagtg	ggggcttggg	26580
ttttttcctt	gggtactggg	tttgtttttc	catgatgagc	atatectatg	atgcactata	26640
gcactcaagc	aagatgcctg	aagcaaagga	ggtgagtcac	catcactggg	ataaaaaaac	26700
aggtcagaga	agtagaagtt	attttctctt	ataattttaa	attttgcctt	aagctcttct	26760
tttgaaatgt	tctaggccaa	agtaatgatt	catggattca	gcacactttc	ctttgttgaa	26820
aagcactgct	tgttccccct	caaagctatg	tgagaggctg	tgtaggagag	agtggagagc	26880
aggtagccta	ccggacctac	agttcaccat	ttcagccctg	taattgacca	gctgtgggac	26940
ctcaggtaag	ctggctaacc	tctctcttac	caatggtaga	tgactatgaa	agctccaaac	27000
tctctcacia	acataggaga	ttattagcat	acaaattaat	gtctagggtt	gtgggtcttg	27060
aggcttcagt	ggaggtcatg	ggcaaagctg	caaagagcat	gggaattaaa	atacatgctc	27120
caggataggc	agtgtgctgg	ctttttctat	ggattaattc	atlttgattct	cacaccaacc	27180
tcaaaaagaa	ggattattag	cccttgatag	atgaggtaac	tgggactcag	agaagttgtg	27240
gagccaggat	tctagatcaa	agcattaaagt	ctttgcttct	gtgctctttc	accttggcca	27300
ggcagctgcc	cttgcccagt	aaatggtaca	tcacagtaag	tgttttatta	aaatgccatt	27360
tccttgaaac	aaagaaatga	tggtattagg	gggagggcaa	gggagacatt	ttgagaatat	27420
ttaagtatat	atgatgacta	tttcttcttc	aaatatctat	ctggtataaa	actactattc	27480
tgttactcta	attatttttt	gaccatagga	gagactgcga	cagaaattcc	attagtggat	27540
ttgagattga	gtttagaata	tttatttaag	tagagctaag	tgtggcaata	tctgtcatat	27600
ctattagttt	ggagaaatga	agaagctttt	ttagttatag	atccagacac	caatgctaata	27660
accaaatact	acagccagtg	ttcttctgtc	gccatagttg	ttacaagtat	gacagcctcc	27720
caagtcattt	attgattcaa	ctcccttttt	gttttaaatgt	tgacacacta	gtttgtatga	27780
acaatgagca	cactagctca	gaagaggaca	acaagaatta	gcgcggatgg	ttcttccccct	27840
tgaggggggtg	ctctgtcagt	atgaacatgc	cttcatgggc	agaaattagg	agcccactag	27900
ctgttaaatga	agagtgcctt	gcttttcctt	cagacagcag	tttccaaagt	tcctcttctc	27960
ctttaatggc	attgcccttt	agtgtgtgtt	aacctgtggt	ttgaaagaaa	tactcgtgta	28020
tattagcaat	tgaataataa	gtgattaaat	taaattacat	ttatcaataa	aaatagctat	28080
tatcgatagc	tgaatgcata	aagtatgcag	catcacatac	ggatgaactc	accgtttgtc	28140
gtgctactac	aggtacatgc	tctacaaaaca	cagaaattct	gatattctat	gaaacattat	28200
taaattccaa	ttgaacatga	tcattccaat	caaataaggg	gaaaaaatat	aaagtatttg	28260
taatcaaaga	ccctgtattg	ttgagtatat	tcctgaaggg	gaggggtttg	ttttgtctag	28320
gattgatata	aagtgaatta	tctgcttatg	atttttcact	ctgattattg	gaataaatatt	28380
ctccacacta	gctcctggat	ctgtgcattt	caaccttgct	tcttccatac	ctgcatcatt	28440
ttgggtattgt	gtatattagg	acacattctg	atlttctgcat	cagaacgctg	agtgagtgtg	28500
cacagtaagc	aaaggagtat	acctggggagc	cagtctcaca	ccaggatggc	tagtaaaaaac	28560
agaaccattc	ataacataac	tgtcaaccaa	taaaatacat	atcactaaaag	ctaaactaaa	28620
ttcgagtacc	ctcaactcaa	cttccccccag	ccacatctca	aaaacatgac	tagctactcc	28680
aacatcaccc	aatataagga	gaactgtaaa	gaaataaagt	cagagtggaga	gaaaaaaaag	28740
cagtcctaata	caacttgatt	aaatatatga	cttcacagca	aattgcataa	aactatatga	28800
ccacatgagc	acattcctag	gccctcccaa	ggccctgaaa	aaagcctgaa	ctagggaggg	28860
gctctaatta	gcttaatgat	acacttacct	atgattgtgg	ttatgtcttg	atlttatctga	28920
ttggcattgt	tttttaaatt	atctaaaagt	gttcatcctt	atlttttaggt	tagcaactgt	28980
gaccctagt	actagtaaca	gtaacaaatg	aaagaagatg	ctcttgatg	gccaaaacga	29040
tgaacagac	ctacatgatt	ttatgaaaag	ttttccttgg	ctttggttca	aagagatttt	29100
tctttccttg	acactaaagt	ggtagtttgc	actaggcata	tagataccgt	tctatctttc	29160
tggttctcca	cttaaatgac	actcatgtct	gctacattaa	aattagcttg	ttaggtttta	29220
tttcaccaag	tttataaagt	aaaccacata	tcgttttctc	ttttgtagat	gctgaaagca	29280
aagttcatgt	gggaaatgtt	tggcaatagc	tgattttatcc	tcagggtaac	aatattctat	29340
aactcctttg	atcttgaggc	ctctgtgatg	gaaatgcttg	gagaaaggga	ttttaaaggg	29400
agattctgaa	gtccttggga	aagtccacaa	gtggacgggg	cttcatagcc	atgacaacaa	29460
atgacattgt	ctaggaaaca	gtgagtcatg	gcatgctgag	cttagaatgg	agccaacaga	29520
aggaacctgg	cctcggacac	agaatctttt	ggctgctgac	ccagaatgac	tgtgaaagac	29580
taacactgtt	tagcagattt	ttcttgagt	tttactatgt	gtgaggttcc	tgggattcag	29640
attcagctac	tattgttaag	aggaaatcaa	ccaggaagtc	agttaaagaa	aggtacagt	29700

ggttttcagg	ctgcagggta	cagaaatggt	cccaggcctg	gagaacaaac	cttcagatct	29760
taatctgtac	agggaggtgg	agggtgaaag	aatgatcttt	caggaagcgt	tcaagtaggg	29820
ctgctgcttg	gattgaattt	taaagaatgc	atagggtata	tgcaggatct	atatatagat	29880
caatagcttc	cctgagcaca	tgttcaaagg	ttcaaacatt	tggggtcatt	tctttgcaag	29940
aagagtcact	cagtggcctg	aaagtccatg	cagcaacttc	cctcatgaga	gctgcttccg	30000
cagcaggccc	agggtttcta	aaggagagag	cacacagatg	taaacactct	gtggttctga	30060
ggactgtcac	ctcttctttt	cacccatcac	ttttgtctta	agaactctat	gctcaaccct	30120
aattctcagt	ctctatatca	attcccacca	aacagatgca	aagtcctgtc	catttgcttc	30180
catgaactct	gtacttatcg	atgatataat	actctgctga	ctacatttta	cttgccactt	30240
catatcctca	ctagactgaa	agacctataa	gggaagagat	atcttattta	tatatctttc	30300
ttatatatct	ttcccatata	tcctattttac	tgttgtaact	acaactccta	caaccgtgct	30360
tggtacatag	gggtgtgaaa	aagtattttat	gaaattatga	ataacactga	ttctattaaa	30420
taacattatt	aagttaatga	acaaataatt	aagcttagta	aaatatcaaa	agttaaagat	30480
atcaaaaaact	aaacacttat	agaataaaaag	tttgcttttc	ttgtctagt	agcacattaa	30540
tacgagtttt	aaccctcttt	tgtcctctcc	tgattcacac	gaaaaaatat	ataggcctca	30600
gctgttcatt	gggtgccagat	aaaaataaag	tactttttta	ttgtaattac	tgcaaaggct	30660
cttcaacagt	gcacagtata	ccaggaactg	aaacttttct	tataaaacaa	aataaatatc	30720
agtagaaaca	gagcaaaggc	atttcattaa	gtattatgga	ctgaattgca	ttccctgtaa	30780
atgtgttaaa	gtctgaactc	tcagtacacc	tcagaatata	actgtattta	gaaatagggc	30840
ctttaaagag	gtagttaaga	ttaaatgaga	tcagtgtgat	tgggtctaat	ctaagatgac	30900
tggtgtcatt	ataagaagag	gagaagacac	cagagatgca	accgcacaga	gaaaaggcca	30960
tgtgagcagg	gatccccaac	ccctgagcca	agaactgaca	gtgggtccatg	gcttgttagg	31020
aaccatgcca	cacagcagga	ggtgagccaa	aggcaaggga	gcaaagcttc	atctgtattt	31080
atagccgctc	cccattgtct	acattacctc	ctgagctctg	cctcctgtcg	gatcagtggt	31140
ggcatttagat	tctcatagga	gtgcacaccc	tattgtgaac	tgcgcatgag	agggatctag	31200
attgcatgct	ccttataaaag	tctaattgcct	gatgatctga	ggtggagctg	aggtgggtgat	31260
gctagctctg	aggagtgggt	gcaaacacag	attaacatta	gcagagaggt	ttgactgccc	31320
agagaccata	ataaatcagt	tgctgcaga	cgcatatcaa	aaccctgtca	gtgagtggca	31380
gggtgataatt	cagctgcacg	tggtggctgg	ctttatagtg	gcaagtgcgt	tgatgtactt	31440
caactgtaca	gctgcacctg	gttgcgtggc	ttatagtggc	aagtgagttg	atgtacttca	31500
actgtacagc	tgcatctggg	ggcaggcttt	aagtcagaat	ctgacactta	ttttagtcca	31560
tgtgtgtcct	gcccattatt	ttatttgtca	cttccatccg	cacctctttc	ctgcactgca	31620
cacttgtctc	aatcagtttt	ggtaagccca	caagctaacc	ctagccaaaa	tgaataaaaa	31680
caatcatcac	tggagagttt	ctttgaaaag	tgggaaagaa	ccaatgatga	gacagcagaa	31740
gactctaaga	ctgccaacaa	aaagaaagct	gcatttaaaa	gaaaataactg	gccgggcgcg	31800
gtggctcatg	cctgtaatcc	caggactttg	ggaggccgag	gcgggcggat	cacgaggtca	31860
ggagattgag	accatcctgg	ctaacaaggt	gaaaccccg	ctctactaaa	aatacaaaaa	31920
attagccggg	catggtggcg	ggtgtctgta	gtcccagcta	ctcaggaggc	tgaagcagga	31980
gaatggcgtg	aacctgagag	gcagagcttc	cagtgaagccg	agatcgtgcc	actgcactcc	32040
agcctgggtg	acagagcgag	actccatctc	aaaaaaaaac	aaaaaaaaac	aaataccatg	32100
agtcctactt	aaattacagg	gtcattgcac	cagataattc	acattctcca	agccctcttt	32160
ttataatatg	tggtgggttg	ctatgcaatg	aagccatgaa	accttcagaa	ctgcttcaact	32220
gcatggaaac	caagcaccct	gtgttaaaac	agactttgga	gtttttcaaa	agaaaaaaaa	32280
aagatgaaca	agaagaacag	aagcaattat	tgaaggccac	cattttatca	aatgtgtctg	32340
tactgacagc	atcatatcat	tcgtagtggc	taaccacatt	gctaaagtta	agaagccctt	32400
tgtatttggt	gaagagttga	ttttgcctgc	tgctaagggt	atatgtcatg	aactttcagg	32460
agaggctgca	gttcaaaagg	tggcatgtgt	ttctcatttg	gctagcacat	aactaaatga	32520
ttagatgaaa	tagcagagaa	tgttgaggta	caattgttac	agagagttaa	tgagccaccg	32580
cagtacatga	ttcagggtga	tgagtctacc	aatgttggtg	aggcaacaat	gcttactttt	32640
gtgcaatata	tttttcagaa	gatgtgcatg	aggatatggt	atgtgcactt	ttgttgccaa	32700
ctaataccat	agctgcagaa	ctattcaagt	ctttgaatga	ttgcatatca	ggaaaactca	32760
attggtcatt	ttgtgtcagt	atatgcatgg	acggaccgac	tgccatgact	ggacagcttt	32820
ctggtttcac	tacttgggtc	aatgaggtca	cttctgaatg	taactcttca	cactgtgtca	32880
tccgtagaga	aatgtcggct	agccaaaaaa	tgtcacctaa	atttaacaat	gttttgcaag	32940
gtgtgattaa	aattattaac	cacattaaag	tgcattgcct	taactcatat	ctgttcacac	33000
agctctgcaa	ggtagtgac	acagagcaca	cagctctctc	ttatatacat	aagtgagatg	33060
gcttttctaaa	ggtagatcac	tggccagagt	gtttgagtta	tgagagccac	tccagagact	33120

tcttttagaa	aaacagacac	cactggcagc	acatttcagt	gacacagaat	gggttaaaaa	33180
acttgcttac	ttgtgtgaca	tattcaacct	gttcagggaa	ttcaatcttt	cacttcagag	33240
gaaaatgaca	gctgtgttca	agttggcaga	tagaggggct	gcattcaaag	ccaaagtgga	33300
attatggggg	caacaagtga	acagtgagat	ttttgacatg	ttccaaaatt	agcaaagatt	33360
ttgaaaaaga	ctgagccatg	gccttctttc	tcccagctag	tgcatgatca	cctgtctcag	33420
ctttcaaaaag	agtttaagca	ttatttttcta	actacaaaag	accctagaac	tggaaggaa	33480
tgaatctgtg	accattttgt	gaataagcca	agtgaactga	ctttgtccat	cctagaagag	33540
gatcaactgc	ttgagatggc	aaatgacaat	gcccttaaaa	gtatgtttga	gacaacttca	33600
aatctccata	cattctggat	taaagtcaag	gtggaatatc	ctgagattgc	cacaaaagta	33660
ctgaaaaatcc	tgcttccatt	tccaatatcc	tatctttgtg	aagtagggtt	ttctgcagcg	33720
acagcaacca	caatcagatt	atggagtaga	ctggacataa	gcaatatact	gcaggtgtca	33780
ctgcctccca	tcacctgcac	atgggactat	ctagttgcag	gaaaacaagc	ttagggtctc	33840
cactgattct	acattatggt	gagttgtata	attatttaat	tatatataat	taattatttta	33900
attatatata	attaattatt	taattataca	tatataatta	tatataatta	aatatatatt	33960
taattatata	atatataaaa	atatataaatt	atttaattat	atatatggcg	agttgtataa	34020
ttatatatta	taaatgtaat	aataatagaa	ataaagtata	caataaatgt	aaatgcactt	34080
gaattatccc	taaagcatcc	ccttatccca	atccacagaa	aaatagtctt	ctatgaaatt	34140
ggtccctggt	gccaaaaagg	ttgggggcca	ttgcatgtga	ggacacaatg	agaaggcaac	34200
tatcttcaag	ccaaggagag	agtcctcaga	aaaatatcaa	acctgttgaa	accttgatct	34260
tggacttcca	gcctctagaa	ctgtgagaaa	ataaattcct	gttgtgtgaa	ccaccagtc	34320
tgtggcattt	tgttacagca	gccctagcaa	actaatatat	tcagcaattc	tttttttttt	34380
ctaggacata	aacatatttt	aatgtcctac	ttcctgggga	gaaatccttt	taattatttt	34440
tgtgtatttg	gaaatagggg	ttgtattcca	aattgtagtc	taccataaag	aactacctga	34500
ggctgggtaa	tttataagga	aaagagggtt	aattgactca	caattctgca	ggctgtacag	34560
gaagcatggc	tggaagcca	caggaaactt	ataatcatgg	tagaagggtga	aggggaaaca	34620
agcacatctt	cacatgggtga	caggagagag	agagatgtaa	tggggaagtg	ccacacactt	34680
ttacaccacc	agatctcatg	ataattcact	gtcatgagaa	gagcaagggg	gaaatccatc	34740
cccatgactt	aatcacctca	caccagggtac	ctcccccaac	actgggaatt	acaattcaac	34800
ttgggatttg	ggtggggaca	cagagccaac	cataacaggg	atatattata	ataaaacgta	34860
ctgagaggta	cacaacagca	ccctggaata	ttgctgccaa	aaatggacct	aatcataagg	34920
aaacatcaga	taaattcaaa	ttgaggaatt	gttcagaat	aaacaagact	aaagcaacat	34980
gacaactaaa	tgcaatactt	gaatctgcat	tggtacctga	aacagtttta	tctatctatc	35040
catccattta	tccaccata	acggtaaagg	atattattgg	gataattgtc	ataatttgaa	35100
taaaatctat	agattaggta	ttagcattac	atcaccatta	atttcctagt	tttgatagtt	35160
gtattctgct	tttataagag	aattttcttg	ttcttaggaa	atactggata	atctgggcaa	35220
aaaaattctg	gaattcttta	gactcttctt	tcaacttttc	catataagtt	ttaagtttat	35280
ttcaaagtat	gaatgctata	aaattaggaa	ttcaaacaaa	aataatcaaa	ttgagagggtg	35340
tgtacattta	acaaaacagt	tatattaaat	caggttaaat	tttaagcatg	ctgaaaattt	35400
gctgagacct	gggagtgttt	gtttctgcca	gtgttagttt	caaagtgcac	agtggcatat	35460
tgaattttgt	gtaattttcca	gtaacataga	gcaaggatga	gtagccacac	acatttagtg	35520
ttgcaataat	ataaaaagcc	tcaggagcac	tccagcgagc	acaacaagtc	cccagggaca	35580
gctaagcact	ccagtgtcta	gggactgtgg	gaaactggaa	agaaacaatc	cagtgtaaat	35640
atgacttcta	agctggctgt	tgctctactg	ctttcttggc	agttgcatgc	tttctgtagc	35700
actgtgtgaa	ggtaggctca	tctttctaata	caatagagtt	ttcttttgtc	taaatatgat	35760
tctccgaaag	caaggctatc	caaaatgctt	tgagatttgc	ttattaaaac	aaaaaaaaat	35820
ccccatttgc	attcatttga	tgttgtcatg	agtacaaaat	aacttttgtg	ggccttagac	35880
atttttacct	ttgtgggact	cttcagccat	cataatatca	atacttaaaa	tttttttatg	35940
taacttagaa	tgcttcaaca	ttttttctgt	tttaggtaaa	atthagggga	tttttatggg	36000
ccctaaaaat	ttctttattt	ctgttgtgag	aaaaaaataa	cactttctta	gattctaaaa	36060
cttcatgttt	ttcttccgac	tttaaaggca	attaaaacaa	tttcatgggc	ttctaaaaat	36120
attgtggggc	ctaggcacta	tgccactagg	ccctaagtga	taagttaccc	ctaatttgca	36180
ttaaatttgg	aattattttag	gttctatctc	tatacctctc	agaaaagtgt	aatatttgca	36240
ttgatgtaga	catttagttg	ctaaaattca	caacttgtcc	tataacacat	atatcactat	36300
atatacttat	attcatttat	aatttatatt	atattccatt	ggggggcaca	gttggttaat	36360
attgctgtt	aaaattgaac	taggtaacca	cgtattttta	ctcagtgttc	tgctgacaaa	36420
ggcttagaca	gtaatcattt	tctgcctgct	ttgaagagtt	ttgatgggcc	ctagaccatc	36480
ttaagatcct	gctatataac	aaatagtgtg	tttttagcat	gcgttttctg	tatttgcttt	36540

tctgttttat	cagcattaaa	agtttttttt	taaaaaaaaa	acaagtcac	tctgtaaaaa	36600
agtcattgtt	ctgtttattc	tttctgaagg	tgatatatct	gttgataaga	tcattgttta	36660
tctcctataa	ataacattat	agcatcatga	agaatactgc	aaaatcaa	agaagaatgg	36720
ccatatggat	ataaaatatt	aatttttaata	aattttatagt	tttatgtatt	tatatattta	36780
tatattagtt	tttatattga	cattcaaaa	agtcagtgag	aatcattttg	aaagaaagga	36840
aattaatttc	aagggttggt	ctaaaactag	tctttctatt	tgtagcaacc	tgtttcgtta	36900
agacatttct	catggtccta	aaaatcatca	tattcaaatt	taaagggtat	ctagcagagt	36960
tgtgcccttt	gatgaaagca	gtccttactt	ccttgctatg	ttcactgctt	ccattgtgcc	37020
aagtattagt	acagtaccac	aatgccagtg	catgaggaca	cattttatac	ctttgcatcc	37080
caaattttat	aaagaactca	gaattattca	gagtgagatta	tattataaaa	attaagaaat	37140
catgtaagta	ctttcaaaa	ttcttagtta	ttttgcttct	gtacatgtag	actgtttagg	37200
tgctgagagt	acaatggtaa	acagaacagc	aaaaaaaaaa	aattctgtct	ttacaaaata	37260
cttggtactg	acatctgggt	agtttttagct	attgtgtctc	ccttgcttct	gaattccaga	37320
gcaatacttt	cattttttga	tataagcaaa	ttctaaaaca	cattgtgggg	aggtagataa	37380
tctgacattt	tgcagagtta	aagtaattag	agaagcacia	gaaagtttcg	aaaatgataa	37440
ttaaatttga	aataggaatt	agcatgagtg	aagcaactcc	aggtacatgg	tgattaaccc	37500
aagtaatatg	actccaggta	tcctgggaat	tcctttcact	gtgaaagctg	caatcagtgg	37560
cctttggaaa	agtaagtggg	gttctctgag	ctcccagaaa	attgtgaaaa	aatcctgttg	37620
ggatcatttc	cattttaccac	tgagccaaat	gaccatgatt	tccaactgca	aagggatatc	37680
taaaaccaga	taagtaattt	acctaagtag	tctttttcac	tcttttagtgt	gaagcttatt	37740
catgaagaga	cctctgcctg	aacatacagc	aaattttaaga	aggttgtgca	gatagtctga	37800
aggagggtgag	ttagtttttc	ccacttttctc	aaattttctca	aattttcattt	gtcatgaaac	37860
taataggaaa	gattcacaaa	tgtcagttta	agagttttac	ctaattggaat	ctcactttta	37920
tttatttttt	tgcttctatt	taaaagcttt	tttttcaatg	atagaaaaaa	tgctagcgat	37980
agtaatttgc	ttttttaata	atggaaaatg	tagagcaata	tagcaaacct	caaagagtat	38040
tgattttctca	aaacaaaagc	ataacaaaa	ttgtttattc	tcttttaatt	tatggtttta	38100
aaaattttac	ttgtatttag	aaataaggaa	aaatgaataa	gaaaaaatta	aagagcattc	38160
ttccatgggt	tccaagaatt	tcttattaaa	tatgttaaca	aaactcgaag	tgaataaaa	38220
ttagagctat	agcctatgct	attggatacc	caccatatac	atctgatctg	caccacttca	38280
atgctcactg	ttttgtcttc	caagggtctt	ctctgggtac	cagcgtccac	tatactagca	38340
aggcccaggt	tggaatattt	ggaaaattaa	tggccttggt	cgcagtcttt	aactaatgac	38400
ccactaaagc	agtgtactgt	aagtcctcac	ttaacctcat	caataaattc	ttggaaactg	38460
tgactttaaa	tgaaatgaat	agcaaaacag	atttttattat	aacttatttg	atagaaataa	38520
tagttaagtt	tctaaggcat	atttctagtc	acaaaacatc	atcaaactgc	caaataaaga	38580
tcaaaataat	tctaataatta	aacactgaaa	tatatgtgaa	ctatatatac	atttcgga	38640
gattaataaaa	agaagataaa	ttactcaatt	tttgggtgaat	ctgtgagtga	caaagggtcat	38700
agtagtggtg	ggtgatgtgg	ggagggtatg	ttactcctta	tcctagttag	gagtaaaccat	38760
gagtcctcca	atatccacac	cctgtctgtc	atcatcaaat	ctcttaaaat	atctagtttt	38820
gtttctaatg	tcacactttt	tctctgggtg	gtgtgtgtgt	ggccatagac	gtaagaagag	38880
gtggatagtg	caacttttaa	gtttattaca	acaaagttaa	gtcagggaat	gaatatgtaa	38940
gaagcacccc	ctaccagtat	ataattcaaa	aacaaacata	aaaaatatgg	tgccctccct	39000
gagctcatac	gatatctttt	attgtcatgt	acttgtatga	ttattgtata	ctttatatct	39060
ttttattttt	tcattaatac	ataatagatg	tacatatttt	ggggatactt	gtgataatct	39120
gatacattca	tgatatgggt	tggtgttttc	cccatccaaa	tctcatcttg	aatttcagtt	39180
cccataatcc	ccatgtgtcg	aggaagggtg	ccggtgggtg	gtaattgaat	catggggggtg	39240
atttccccc	tgctgttctc	ctgatagtga	atgagttatc	atgaggtctg	atgggttttac	39300
aagaggcttc	ccctttgact	tggcactcat	tctctgtcct	gccgtccgt	gaagagggtg	39360
attctgccat	gattgtgaag	ttcctgaggt	ctccccggcc	ctgccgaact	gtgagtcaat	39420
tatgcctctt	ttctttataa	attgcccagt	ttgggggcag	ttttttatag	cagtgtgaga	39480
ctgaattaat	acaatcaaat	cagggttaatt	gggatgtaca	tcaccttaaa	tacttttctt	39540
tgtgccagga	acatttgaat	tattctcttc	tagctatttt	gaaatgtaca	atagattgac	39600
ttaccctact	gaactatgga	acacaatgtc	ttatttcttt	caattaaactg	tatagttgtc	39660
ctcactattc	aatctctgtt	cttcctcttc	acttccaaca	attcttggcc	ttggtaacca	39720
tcaatctact	ctctatcttc	atgatatcta	cttttgtgtc	tcccacatat	gagtgagaat	39780
aggccatatt	tgctctctctg	tgcttggttc	atttcactta	acataatgac	ctccagttcc	39840
atctatgttg	ctgcaaatga	caggattgca	ttagttgttg	tggtgaaaa	atattcaatt	39900
atgtatatat	accacagttt	ctttatacac	tcattccattg	atggacactt	aggttgatta	39960

catattttgt ctattgtgaa tagtgctgca ataaatatgg gattgcagat acctctttga 40020
tataccgatt ttctttcttt tggatatata cccagtagtt aattgctggg tcatgtgtag 40080
ttctattttc agtttttggg ggaacctcca taccgttttt catagtgggc attttaattt 40140
actttcccac caacatgtat gaggggtttcc ctttctctcc atcctcgcca gcatctgtta 40200
ttacctgtca ttttgataaa ggccattgta agtgggggta gatgatatct cattgtgggt 40260
tggatttgca tttttctggg gactagtgat gttgagtatt tttttcatat aactgttggc 40320
catttgatg ccttcatttg agaaatgtct gttcagatct gttgtccggt ttaaaatcag 40380
attattttgt tttgcgctat tgaattgttg gagctcctta tatattcttg ttactaatac 40440
ttgtgaaatg gatagtttat aaaaattttc tcccattctg tctctttact ttggtgattg 40500
tttttcttgc tgtgcagaag ctttttagct ttatgtaatc tcaattgtca atttttgttc 40560
ttattgacctg tgctttgccc agcccaatgt cctagaatgt ttccccaatg ttttcttcta 40620
gtagcttcat agtttcagggt cttagattta agtcctttaat tcattttgat tacatttttg 40680
tatagcctga gacatagggg tctaatttca ctctatgcat atgggtatcc agttttccca 40740
gcaccattta tgaaagagac tgcccttccc ccattgtcta ttcttggtgt ctttgtaaaa 40800
aatgacttgg ctataaatgt gtttattgat atctgggttc tctattctat tccattagtg 40860
tacatgtctg tttttctacc aaccatgcta atttggttac cataccttg tagtatgttt 40920
taaagtggga tagtgtgatg cttccagctt tgtgtttttt actcaggatt gctttggcta 40980
ttcaggaat ttttttagtgt gtggttctat gtaaatttga gaattttttt ctatttatgg 41040
gaagaaagtc agaattttga cagggattgc attgaatctc taaattgctt gtcattcttg 41100

<210> 47
<211> 85
<212> PRT
<213> Homo sapiens

<400> 47
Met Thr Ser Lys Leu Ala Val Ala Leu Leu Leu Leu Gly Ser Cys Met
1 5 10 15
Leu Ser Val Ala Leu Cys Glu Val Pro Ser Ile Ser Thr Val Pro Gln
20 25 30
Cys Gln Cys Met Arg Thr His Phe Ile Pro Leu His Pro Lys Phe Ile
35 40 45
Lys Glu Leu Arg Ile Ile Gln Val Leu Ser Lys Val Leu Ser Tyr Phe
50 55 60
Ala Ser Val His Val Asp Cys Leu Gly Ala Glu Ser Thr Met Val Asn
65 70 75 80
Arg Thr Ala Lys Lys
85

<210> 48
<211> 91
<212> PRT
<213> Homo sapiens

<400> 48
Met Thr Ser Lys Leu Ala Val Ala Leu Leu Ala Ala Phe Leu Ile Ser
1 5 10 15
Ala Ala Leu Cys Glu Gly Ala Val Leu Pro Arg Ser Ala Lys Glu Leu
20 25 30

Arg Cys Gln Cys Ile Lys Thr Tyr Ser Lys Pro Phe His Pro Lys Phe
35 40 45

Ile Lys Glu Leu Arg Val Ile Glu Ser Gly Pro His Cys Ala Asn Thr
50 55 60

Glu Ile Ile Val Lys Leu Ser Asp Gly Arg Glu Leu Cys Leu Asp Pro
65 70 75 80

Lys Glu Asn Trp Val Gln Arg Val Val Glu Lys
85 90

<210> 49
<211> 85
<212> PRT
<213> Homo sapiens

<400> 49
Met Thr Ser Lys Leu Ala Val Ala Leu Leu Leu Leu Gly Ser Cys Met
1 5 10 15

Leu Ser Val Ala Leu Cys Glu Val Pro Ser Ile Ser Thr Val Pro Gln
20 25 30

Cys Gln Cys Met Arg Thr His Phe Ile Pro Leu His Pro Lys Phe Ile
35 40 45

Lys Glu Leu Arg Ile Ile Gln Val Leu Ser Lys Val Leu Ser Tyr Phe
50 55 60

Ala Ser Val His Val Asp Cys Leu Gly Ala Glu Ser Thr Met Val Asn
65 70 75 80

Arg Thr Ala Lys Lys
85

<210> 50
<211> 91
<212> PRT
<213> Homo sapiens

<400> 50
Met Thr Ser Lys Leu Ala Val Ala Leu Leu Ala Ala Phe Leu Ile Ser
1 5 10 15

Ala Ala Leu Cys Glu Gly Ala Val Leu Pro Arg Ser Ala Lys Glu Leu
20 25 30

Arg Cys Gln Cys Ile Lys Thr Tyr Ser Lys Pro Phe His Pro Lys Phe
35 40 45

Ile Lys Glu Leu Arg Val Ile Glu Ser Gly Pro His Cys Ala Asn Thr
50 55 60

Glu Ile Ile Val Lys Leu Ser Asp Gly Arg Glu Leu Cys Leu Asp Pro
65 70 75 80

Lys Glu Asn Trp Val Gln Arg Val Val Glu Lys
85 90

<210> 51
<211> 55
<212> PRT
<213> Homo sapiens

<400> 51
Met Thr Ser Lys Leu Ala Val Ala Leu Leu Leu Leu Gly Ser Cys Met
1 5 10 15

Leu Ser Val Ala Leu Cys Glu Val Pro Ser Ile Ser Thr Val Pro Gln
20 25 30

Cys Gln Cys Met Arg Thr His Phe Ile Pro Leu His Pro Lys Phe Ile
35 40 45

Lys Glu Leu Arg Ile Ile Gln
50 55

<210> 52
<211> 58
<212> PRT
<213> Homo sapiens

<400> 52
Met Thr Ser Lys Leu Ala Val Ala Leu Leu Ala Ala Phe Leu Ile Ser
1 5 10 15

Ala Ala Leu Cys Glu Gly Ala Val Leu Pro Arg Ser Ala Lys Glu Leu
20 25 30

Arg Cys Gln Cys Ile Lys Thr Tyr Ser Lys Pro Phe His Pro Lys Phe
35 40 45

Ile Lys Glu Leu Arg Val Ile Glu Ser Gly
50 55

<210> 53
<211> 56
<212> PRT
<213> Homo sapiens

<400> 53
Met Thr Ser Lys Leu Ala Val Ala Phe Leu Ala Val Phe Leu Leu Ser
1 5 10 15

Ala Ala Leu Cys Glu Ala Asp Val Leu Ala Arg Val Ser Ala Glu Leu
20 25 30

Arg Cys Gln Cys Ile Asn Thr His Ser Thr Pro Phe His Pro Lys Phe
 35 40 45

Ile Lys Glu Leu Arg Val Ile Glu
 50 55

<210> 54

<211> 58

<212> PRT

<213> Homo sapiens

<400> 54

Met Thr Ser Lys Leu Ala Val Ala Leu Leu Ala Ala Phe Leu Ile Ser
 1 5 10 15

Ala Ala Leu Cys Glu Gly Ala Val Leu Pro Arg Ser Ala Lys Glu Leu
 20 25 30

Arg Cys Gln Cys Ile Lys Thr Tyr Ser Lys Pro Phe His Pro Lys Phe
 35 40 45

Ile Lys Glu Leu Arg Val Ile Glu Ser Gly
 50 55

<210> 55

<211> 414

<212> PRT

<213> Homo sapiens

<400> 55

Met Asn Pro Thr Leu Gly Leu Ala Ile Phe Leu Ala Val Leu Leu Thr
 1 5 10 15

Val Lys Gly Leu Leu Lys Pro Ser Phe Ser Pro Arg Asn Tyr Lys Ala
 20 25 30

Leu Ser Glu Val Gln Gly Trp Lys Gln Arg Met Ala Ala Lys Glu Leu
 35 40 45

Ala Arg Gln Asn Met Asp Leu Gly Phe Lys Leu Leu Lys Lys Leu Ala
 50 55 60

Phe Tyr Asn Pro Gly Arg Asn Ile Phe Leu Ser Pro Leu Ser Ile Ser
 65 70 75 80

Thr Ala Phe Ser Met Leu Cys Leu Gly Ala Gln Asp Ser Thr Leu Asp
 85 90 95

Glu Ile Lys Gln Gly Phe Asn Phe Arg Lys Met Pro Glu Lys Asp Leu
 100 105 110

His Glu Gly Phe His Tyr Ile Ile His Glu Leu Thr Gln Lys Thr Gln
 115 120 125

Asp Leu Lys Leu Ser Ile Gly Asn Thr Leu Phe Ile Asp Gln Arg Leu

130	135	140
Gln Pro Gln Arg Lys Phe Leu Glu Asp Ala Lys Asn Phe Tyr Ser Ala		
145	150	155 160
Glu Thr Ile Leu Thr Asn Phe Gln Asn Leu Glu Met Ala Gln Lys Gln		
	165	170 175
Ile Asn Asp Phe Ile Ser Gln Lys Thr His Gly Lys Ile Asn Asn Leu		
	180	185 190
Ile Glu Asn Ile Asp Pro Gly Thr Val Met Leu Leu Ala Asn Tyr Ile		
	195	200 205
Phe Phe Arg Ala Arg Trp Lys His Glu Phe Asp Pro Asn Val Thr Lys		
	210	215 220
Glu Glu Asp Phe Phe Leu Glu Lys Asn Ser Ser Val Lys Val Pro Met		
	225	230 235 240
Met Phe Arg Ser Gly Ile Tyr Gln Val Gly Tyr Asp Asp Lys Leu Ser		
	245	250 255
Cys Thr Ile Leu Glu Ile Pro Tyr Gln Lys Asn Ile Thr Ala Ile Phe		
	260	265 270
Ile Leu Pro Asp Glu Gly Lys Leu Lys His Leu Glu Lys Gly Leu Gln		
	275	280 285
Val Asp Thr Phe Ser Arg Trp Lys Thr Leu Leu Ser Arg Arg Val Val		
	290	295 300
Asp Val Ser Val Pro Arg Leu His Met Thr Gly Thr Phe Asp Leu Lys		
	305	310 315 320
Lys Thr Leu Ser Tyr Ile Gly Val Ser Lys Ile Phe Glu Glu His Gly		
	325	330 335
Asp Leu Thr Lys Ile Ala Pro His Arg Ser Leu Lys Val Gly Glu Ala		
	340	345 350
Val His Lys Ala Glu Leu Lys Met Asp Glu Arg Gly Thr Glu Gly Ala		
	355	360 365
Ala Gly Thr Gly Ala Gln Thr Leu Pro Met Glu Thr Pro Leu Val Val		
	370	375 380
Lys Ile Asp Lys Pro Tyr Leu Leu Leu Ile Tyr Ser Glu Lys Ile Pro		
	385	390 395 400
Ser Val Leu Phe Leu Gly Lys Ile Val Asn Pro Ile Gly Lys		
	405	410

<210> 56
 <211> 414
 <212> PRT

<213> Homo sapiens

<400> 56

Met	Asn	Pro	Thr	Leu	Gly	Leu	Ala	Ile	Phe	Leu	Ala	Val	Leu	Leu	Thr
1				5				10					15		
Val	Lys	Gly	Leu	Leu	Lys	Pro	Ser	Phe	Ser	Pro	Arg	Asn	Tyr	Lys	Ala
			20					25					30		
Leu	Ser	Glu	Val	Gln	Gly	Trp	Lys	Gln	Arg	Met	Ala	Ala	Lys	Glu	Leu
		35					40					45			
Ala	Arg	Gln	Asn	Met	Asp	Leu	Gly	Phe	Lys	Leu	Leu	Lys	Lys	Leu	Ala
	50					55					60				
Phe	Tyr	Asn	Pro	Gly	Arg	Asn	Ile	Phe	Leu	Ser	Pro	Leu	Ser	Ile	Ser
65					70					75					80
Thr	Ala	Phe	Ser	Met	Leu	Cys	Leu	Gly	Ala	Gln	Asp	Ser	Thr	Leu	Asp
				85					90					95	
Glu	Ile	Lys	Gln	Gly	Phe	Asn	Phe	Arg	Lys	Met	Pro	Glu	Lys	Asp	Leu
			100					105					110		
His	Glu	Gly	Phe	His	Tyr	Ile	Ile	His	Glu	Leu	Thr	Gln	Lys	Thr	Gln
		115					120					125			
Asp	Leu	Lys	Leu	Ser	Ile	Gly	Asn	Thr	Leu	Phe	Ile	Asp	Gln	Arg	Leu
	130					135					140				
Gln	Pro	Gln	Arg	Lys	Phe	Leu	Glu	Asp	Ala	Lys	Asn	Phe	Tyr	Ser	Ala
145					150					155					160
Glu	Thr	Ile	Leu	Thr	Asn	Phe	Gln	Asn	Leu	Glu	Met	Ala	Gln	Lys	Gln
			165						170					175	
Ile	Asn	Asp	Phe	Ile	Ser	Gln	Lys	Thr	His	Gly	Lys	Ile	Asn	Asn	Leu
			180					185					190		
Ile	Glu	Asn	Ile	Asp	Pro	Gly	Thr	Val	Met	Leu	Leu	Ala	Asn	Tyr	Ile
		195					200					205			
Phe	Phe	Arg	Ala	Arg	Trp	Lys	His	Glu	Phe	Asp	Pro	Asn	Val	Thr	Lys
	210					215					220				
Glu	Glu	Asp	Phe	Phe	Leu	Glu	Lys	Asn	Ser	Ser	Val	Lys	Val	Pro	Met
225					230					235					240
Met	Phe	Arg	Ser	Gly	Ile	Tyr	Gln	Val	Gly	Tyr	Asp	Asp	Lys	Leu	Ser
				245					250					255	
Cys	Thr	Ile	Leu	Glu	Ile	Pro	Tyr	Gln	Lys	Asn	Ile	Thr	Ala	Ile	Phe
			260					265					270		
Ile	Leu	Pro	Asp	Glu	Gly	Lys	Leu	Lys	His	Leu	Glu	Lys	Gly	Leu	Gln
		275					280					285			

Val Asp Thr Phe Ser Arg Trp Lys Thr Leu Leu Ser Arg Arg Val Val
 290 295 300
 Asp Val Ser Val Pro Arg Leu His Met Thr Gly Thr Phe Asp Leu Lys
 305 310 315 320
 Lys Thr Leu Ser Tyr Ile Gly Val Ser Lys Ile Phe Glu Glu His Gly
 325 330 335
 Asp Leu Thr Lys Ile Ala Pro His Arg Ser Leu Lys Val Gly Glu Ala
 340 345 350
 Val His Lys Ala Glu Leu Lys Met Asp Glu Arg Gly Thr Glu Gly Ala
 355 360 365
 Ala Gly Thr Gly Ala Gln Thr Leu Pro Met Glu Thr Pro Leu Val Val
 370 375 380
 Lys Ile Asp Lys Pro Tyr Leu Leu Leu Ile Tyr Ser Glu Lys Ile Pro
 385 390 395 400
 Ser Val Leu Phe Leu Gly Lys Ile Val Asn Pro Ile Gly Lys
 405 410

<210> 57

<211> 361

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)..(361)

<223> Wherein Xaa is any amino acid as defined in the
specification

<400> 57

Asp Leu Gly Phe Lys Leu Leu Lys Lys Leu Ala Phe Tyr Asn Pro Gly
 1 5 10 15
 Arg Asn Ile Phe Leu Ser Pro Leu Ser Ile Ser Thr Ala Phe Ser Met
 20 25 30
 Leu Cys Leu Gly Ala Gln Asp Ser Thr Leu Asp Glu Ile Lys Gln Gly
 35 40 45
 Phe Asn Phe Arg Lys Met Pro Glu Lys Asp Leu His Glu Gly Phe His
 50 55 60
 Tyr Ile Ile His Glu Leu Thr Gln Lys Thr Gln Asp Leu Lys Leu Ser
 65 70 75 80
 Ile Gly Asn Thr Leu Phe Ile Asp Gln Arg Leu Gln Pro Gln Arg Lys
 85 90 95
 Phe Leu Glu Asp Ala Lys Asn Phe Tyr Ser Ala Glu Thr Ile Leu Thr
 100 105 110

Asn Phe Gln Asn Leu Glu Met Ala Gln Lys Gln Ile Asn Asp Phe Ile
 115 120 125
 Ser Gln Lys Thr His Gly Lys Ile Asn Asn Leu Ile Glu Asn Ile Asp
 130 135 140
 Pro Gly Thr Val Met Leu Leu Ala Asn Tyr Ile Phe Phe Arg Ala Arg
 145 150 155 160
 Trp Lys His Glu Phe Asp Pro Asn Val Thr Lys Glu Glu Asp Phe Phe
 165 170 175
 Leu Glu Lys Asn Ser Ser Val Lys Val Pro Met Met Phe Arg Ser Gly
 180 185 190
 Ile Tyr Gln Val Gly Tyr Asp Asp Lys Leu Ser Cys Thr Ile Leu Glu
 195 200 205
 Ile Pro Tyr Gln Lys Asn Ile Thr Ala Ile Phe Ile Leu Pro Asp Glu
 210 215 220
 Gly Lys Leu Lys His Leu Glu Lys Gly Leu Gln Val Asp Thr Phe Ser
 225 230 235 240
 Arg Trp Lys Thr Leu Leu Ser Arg Arg Val Val Asp Val Ser Val Pro
 245 250 255
 Arg Leu His Met Thr Gly Thr Phe Asp Leu Lys Lys Thr Leu Ser Tyr
 260 265 270
 Ile Gly Val Ser Lys Ile Phe Glu Glu His Gly Asp Leu Thr Lys Ile
 275 280 285
 Ala Pro His Arg Ser Leu Lys Val Gly Glu Ala Val His Lys Ala Glu
 290 295 300
 Leu Lys Met Asp Glu Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 305 310 315 320
 Xaa Xaa Leu Pro Met Glu Thr Pro Leu Val Val Lys Ile Asp Lys Pro
 325 330 335
 Tyr Leu Leu Leu Ile Tyr Ser Glu Lys Ile Pro Ser Val Leu Phe Leu
 340 345 350
 Gly Lys Ile Val Asn Pro Ile Gly Lys
 355 360

<210> 58
 <211> 363
 <212> PRT
 <213> Homo sapiens

<400> 58
 Glu Phe Ala Phe Ser Leu Tyr Arg Gln Leu Ala His Gln Ser Asn Ser

1	5	10	15
Thr Asn Ile Phe Phe Ser Pro Val Ser Ile Ala Thr Ala Phe Ala Met	20	25	30
Leu Ser Leu Gly Thr Lys Ala Asp Thr Gln Ser Glu Ile Leu Glu Gly	35	40	45
Leu Asn Phe Asn Leu Thr Glu Ile Pro Gln Ala Gln Val His Glu Gly	50	55	60
Phe Gln Glu Leu Leu Arg Thr Leu Asn Lys Pro Asp Ser Gln Leu Gln	65	70	75
Leu Thr Thr Gly Asn Gly Leu Phe Leu Asn Lys Ser Leu Lys Val Val	85	90	95
Asp Lys Phe Leu Glu Asp Val Lys Asn Leu Tyr His Ser Glu Ala Phe	100	105	110
Ser Val Asn Phe Gln Asp Thr Glu Glu Ala Lys Lys Gln Ile Asn Asn	115	120	125
Tyr Val Glu Lys Gly Thr Gln Gly Lys Val Val Asp Leu Val Lys Glu	130	135	140
Leu Asp Arg Asp Thr Val Phe Ala Leu Val Asn Tyr Ile Phe Phe Lys	145	150	155
Gly Lys Trp Glu Arg Pro Phe Glu Val Glu Ala Thr Glu Glu Glu Asp	165	170	175
Phe His Val Asp Gln Ala Thr Thr Val Lys Val Pro Met Met Arg Arg	180	185	190
Leu Gly Met Phe Asn Ile Tyr His Cys Glu Lys Leu Ser Ser Trp Val	195	200	205
Leu Leu Met Lys Tyr Leu Gly Asn Ala Thr Ala Ile Phe Phe Leu Pro	210	215	220
Asp Gln Gly Lys Leu Gln His Leu Glu Asn Glu Leu Thr His Asp Ile	225	230	235
Ile Thr Lys Phe Leu Glu Asn Glu Asn Arg Arg Ser Ala Asn Leu His	245	250	255
Leu Pro Lys Leu Ala Ile Thr Gly Thr Tyr Asp Leu Lys Thr Val Leu	260	265	270
Gly His Leu Gly Ile Thr Lys Val Phe Ser Asn Gly Ala Asp Leu Ser	275	280	285
Gly Val Thr Glu Asp Ala Pro Leu Lys Leu Ser Lys Ala Val His Lys	290	295	300
Ala Val Leu Thr Ile Asp Glu Lys Gly Thr Glu Ala Ala Gly Ala Met			

305 310 315 320
 Phe Leu Glu Ala Ile Pro Met Ser Ile Pro Pro Glu Val Lys Phe Asn
 325 330 335
 Lys Pro Phe Val Phe Leu Met Ile Glu Gln Asn Thr Lys Ser Pro Leu
 340 345 350
 Phe Ile Gly Lys Val Val Asn Pro Thr Gln Lys
 355 360

<210> 59
 <211> 1090
 <212> DNA
 <213> Homo sapiens

<400> 59
 cggatgctgg cccggaggaa gccgatgctg ccggcgctca ccatcaaccc taccatcgcc 60
 gagggcccgt ccccaaccag cgagggcgcc tccgaggcaa acctggtgga cctgcagaag 120
 aagctggagg agctggaact tgacgagcag cagaagcggc tggaagcctt tctcaccag 180
 aaagccaagg tcggcgaact caaagacgat gacttcgaaa ggacctcaga gctggacgcg 240
 ggcaacggcg ggggtggtcac caaagtccag cacagaccct cgggcctcat catggccagg 300
 aagctgatcc accttgagat caagccggcc atccggaacc agatcatccg cgagcaccag 360
 gtccctgcacg agtgcaactc accgtacatc gtgggcttct acggggcctt ctactgtgac 420
 agggagatca gcatctgcat ggagcacatg gatggcggct ccctggacca ggggctgaaa 480
 gaggccaaga ggattcccga ggacatcctg gggaaagtca gcattgcggt tctccggggc 540
 ttggcgtacc tccgagagaa gcaccagatc atgcaccgaa atgtgaagcc ctccaacatc 600
 ctcgatgaact ctagagggga gatcaagctg tgtgacttcg gggtagcgcg ccagctcatc 660
 gactccatgg ccaactcctt cgtgggcacg cgctcctaca tggctccgga gcggttgacg 720
 ggcacacatt actcgggtgca gtcggtcacg tggagcatgg acctgtccct ggtggagctg 780
 gccatcgaaa ggtaccccat ccccccgcgc gacgccaagg agctggaggc catctttggc 840
 cagcccgtgg tcgacaggga agaaggagag cctcacagca tctcctcttg gccagggtcc 900
 cccgggcgcg ccaacagcgg ttacgggatg gacagcctgc ccgcatggc catcttcgaa 960
 ctgctggact atattgtgaa agagccgcct cctaagctgc ccaacgggtg gttcaccccc 1020
 gacttccagg agtttgtcaa taaatgcctc atcaaaaacc caacggagcg ggcggaccta 1080
 aagatgctca 1090

<210> 60
 <211> 1090
 <212> DNA
 <213> Homo sapiens

<400> 60
 cggatgctgg cccggaggaa gccgatgctg ccggcgctca ccatcaaccc taccatcgcc 60
 gagggcccgt ccccaaccag cgagggcgcc tccgaggcaa acctggtgga cctgcagaag 120
 aagctggagg agctggaact tgacgagcag cagaagcggc tggaagcctt tctcaccag 180
 aaagccaagg tcggcgaact caaagacgat gacttcgaaa ggacctcaga gctggacgcg 240
 ggcaacggcg ggggtggtcac caaagtccag cacagaccct cgggcctcat catggccagg 300
 aagctgatcc accttgagat caagccggcc atccggaacc agatcatccg cgagcaccag 360
 gtccctgcacg agtgcaactc accgtacatc gtgggcttct acggggcctt ctactgtgac 420
 agggagatca gcatctgcat ggagcacatg gatggcggct ccctggacca ggggctgaaa 480
 gaggccaaga ggattcccga ggacatcctg gggaaagtca gcattgcggt tctccggggc 540
 ttggcgtacc tccgagagaa gcaccagatc atgcaccgaa atgtgaagcc ctccaacatc 600
 ctcgatgaact ctagagggga gatcaagctg tgtgacttcg gggtagcgcg ccagctcatc 660
 gactccatgg ccaactcctt cgtgggcacg cgctcctaca tggctccgga gcggttgacg 720

ggcacacatt	actcgggtgca	gtcgggtcatc	tggagcatgg	acctgtccct	ggtggagctg	780
gccatcgaaa	ggtaccccat	cccccgccc	gacgccaagg	agctggaggc	catctttggc	840
cagcccggtg	tcgacagggg	agaaggagag	cctcacagca	tctcctcttg	gccagggtcc	900
ccccggcgcc	ccaacagcgg	ttacgggatg	gacagcctgc	ccgccatggc	catcttcgaa	960
ctgctggact	atattgtgaa	agagccgcct	cctaagctgc	ccaacgggtg	gttcaccccc	1020
gacttccagg	agtttgtcaa	taaatgcctc	atcaaaaacc	caacggagcg	ggcggaccta	1080
aagatgctca						1090

<210> 61
 <211> 1088
 <212> DNA
 <213> Homo sapiens

<400> 61					
gatgctggcc	cggaggaagc	cgatgctgcc	ggcgctcacc	atcaacccta	ccatcgccga 60
gggcccgtcc	ccaaccagcg	agggcgccctc	cgaggcaaac	ctggtggacc	tgcagaagaa 120
gctggaggag	ctggaacttg	acgagcagca	gaagcggctg	gaagcctttc	tcaccagaa 180
agccaaggtc	ggcgaactca	aagacgatga	cttcgaaagg	acctcagagc	tggacgcggg 240
caacggcggg	gtggtcacca	aagtccagca	cagaccctcg	ggcctcatca	tggccaggaa 300
gctgatccac	cttgagatca	agccggccat	ccggaaccag	atcatccgcg	agcaccaggt 360
cctgcacgag	tgcaactcac	cgtacatcgt	gggcttctac	ggggccttct	actgtgacag 420
ggagatcagc	atctgcatgg	agcacatgga	tggcggctcc	ctggaccagg	ggctgaaaga 480
ggccaagagg	attcccagag	acatcctggg	gaaagtcagc	attgcgggtc	tccggggctt 540
ggcgtacctc	cgagagaagc	accagatcat	gcaccgaaat	gtgaagccct	ccaacatcct 600
cgtgaactct	agagggggaga	tcaagctgtg	tgacttcggg	gtgagcggcc	agctcatcga 660
ctccatggcc	aactccttcg	tgggcacgcg	ctcctacatg	gctccggagc	ggttgaggag 720
cacacattac	tcggtgcagt	cggtcatctg	gagcatggac	ctgtccctgg	tggagctggc 780
catcgaaaag	taccccatcc	ccccgcccga	cgccaaggag	ctggaggcca	tctttggcca 840
gcccgtggtc	gacagggaa	aaggagagcc	tcacagcatc	tctcttggc	cagggtcccc 900
cgggcgcccc	aacagcgggt	acgggatgga	cagcctgccc	gccatggcca	tcttcgaaat 960
gctggactat	attgtgaaag	agccgcctcc	taagctgccc	aacgggtgtg	tcacccccga 1020
cttcaggag	tttgtcaata	aatgcctcat	caaaaaccca	acggagcggg	cggacctaaa 1080
gatgctca					1088

<210> 62
 <211> 1091
 <212> DNA
 <213> Homo sapiens

<400> 62					
gatgctggcc	cggaggaagc	cggtgctgcc	ggcgctcacc	atcaacccta	ccatcgccga 60
gggcccattc	cctaccagcg	agggcgccctc	cgaggcaaac	ctggtggacc	tgcagaagaa 120
gctggaggag	ctggaacttg	acgagcagca	gaagaagcgg	ctggaagcct	ttctcaccca 180
gaaagccaag	gttggcgaa	tcaaagacga	tgacttcgaa	aggatctcag	agctgggcgc 240
gggcaacggc	gggggtggtca	ccaaagtcca	gcacagaccc	tcgggcctca	tcatggccag 300
gaagctgac	caccttgaga	tcaagccggc	catccggaac	cagatcatcc	gcgagctgca 360
ggtcctgcac	gaatgcaact	cgcctacat	cgtgggcttc	tacggggcct	tctacagtga 420
gggggagatc	agcatttgca	tggaaacacat	ggacggcggc	tccctggacc	aggtgctgaa 480
ggaggccaag	aggattcccc	aggagatcct	ggggaaagtc	agcatcgcg	ttctccgggg 540
gttggcgtag	ctccgagaga	agcaccagat	catgcaccga	gatgtgaagc	cctccaacat 600
gctcgtgaac	tctagagggg	agatcaagct	gtgtgacttc	ggggtgagcg	gccagctcat 660
ggactccatg	gccaaactct	tcgtgggcac	gcgtccctac	atgggtccgg	agcggttgca 720
gggcacacat	tactcggtgc	agtcggacat	ctggagcatg	ggcctgtccc	tgggtggagct 780
ggcgcctcga	aggtacccca	tcccccgcc	cgacgcaaaa	gagctggagg	ccatctttgg 840
gcggcccgtg	gtcgacgggg	aagaaggaga	gcctcacagc	atctcgccctc	ggccgaggcc 900


```

gcccgggcgc cccgtcagcg gtcacgggat ggatagccgg cctgccatgg ccattcttga 960
gctcctggac tatattgtga acgagccacc tcctaagctg cccaacggtg tggtcaccct 1020
ggacttccag gagtttgtca ataaatgcct catcaagaac ccagcggagc gggcggacct 1080
gaagatgctc a 1091

```

```

<210> 63
<211> 363
<212> PRT
<213> Homo sapiens

```

```

<220>
<221> VARIANT
<222> (1)..(363)
<223> Wherein Xaa is any amino acid as defined in the
specification

```

```

<400> 63
Met Leu Ala Arg Arg Lys Pro Met Leu Pro Ala Leu Thr Ile Asn Pro
  1             5             10             15

Thr Ile Ala Glu Gly Pro Ser Pro Thr Ser Glu Gly Ala Ser Glu Ala
      20             25             30

Asn Leu Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
  35             40             45

Xaa Xaa Xaa Xaa Xaa Xaa Ala Phe Leu Thr Gln Lys Ala Lys Val Gly
  50             55             60

Glu Leu Lys Asp Asp Asp Phe Glu Arg Thr Ser Glu Leu Asp Ala Gly
  65             70             75             80

Asn Gly Gly Val Val Thr Lys Val Gln His Arg Pro Ser Gly Leu Ile
      85             90             95

Met Ala Arg Lys Leu Ile His Leu Glu Ile Lys Pro Ala Ile Arg Asn
      100            105            110

Gln Ile Ile Arg Glu His Gln Val Leu His Glu Cys Asn Ser Pro Tyr
      115            120            125

Ile Val Gly Phe Tyr Gly Ala Phe Tyr Cys Asp Arg Glu Ile Ser Ile
      130            135            140

Cys Met Glu His Met Asp Gly Gly Ser Leu Asp Gln Gly Leu Lys Glu
      145            150            155            160

Ala Lys Arg Ile Pro Glu Asp Ile Leu Gly Lys Val Ser Ile Ala Val
      165            170            175

Leu Arg Gly Leu Ala Tyr Leu Arg Glu Lys His Gln Ile Met His Arg
      180            185            190

Asn Val Lys Pro Ser Asn Ile Leu Val Asn Ser Arg Gly Glu Ile Lys
      195            200            205

```

Leu Cys Asp Phe Gly Val Ser Gly Gln Leu Ile Asp Ser Met Ala Asn
 210 215 220
 Ser Phe Val Gly Thr Arg Ser Tyr Met Ala Pro Glu Arg Leu Gln Gly
 225 230 235 240
 Thr His Tyr Ser Val Gln Ser Val Ile Trp Ser Met Asp Leu Ser Leu
 245 250 255
 Val Glu Leu Ala Ile Glu Arg Tyr Pro Ile Pro Pro Pro Asp Ala Lys
 260 265 270
 Glu Leu Glu Ala Ile Phe Gly Gln Pro Val Val Asp Arg Glu Glu Gly
 275 280 285
 Glu Pro His Ser Ile Ser Ser Trp Pro Gly Ser Pro Gly Arg Pro Asn
 290 295 300
 Ser Gly Tyr Gly Met Asp Ser Leu Pro Ala Met Ala Ile Phe Glu Leu
 305 310 315 320
 Leu Asp Tyr Ile Val Lys Glu Pro Pro Pro Lys Leu Pro Asn Gly Val
 325 330 335
 Phe Thr Pro Asp Phe Gln Glu Phe Val Asn Lys Cys Leu Ile Lys Asn
 340 345 350
 Pro Thr Glu Arg Ala Asp Leu Lys Met Leu Ser
 355 360

<210> 64
 <211> 364
 <212> PRT
 <213> Homo sapiens

<400> 64
 Met Leu Ala Arg Arg Lys Pro Val Leu Pro Ala Leu Thr Ile Asn Pro
 1 5 10 15
 Thr Ile Ala Glu Gly Pro Ser Pro Thr Ser Glu Gly Ala Ser Glu Ala
 20 25 30
 Asn Leu Val Asp Leu Gln Lys Lys Leu Glu Glu Leu Glu Leu Asp Glu
 35 40 45
 Gln Gln Lys Lys Arg Leu Glu Ala Phe Leu Thr Gln Lys Ala Lys Val
 50 55 60
 Gly Glu Leu Lys Asp Asp Asp Phe Glu Arg Ile Ser Glu Leu Gly Ala
 65 70 75 80
 Gly Asn Gly Gly Val Val Thr Lys Val Gln His Arg Pro Ser Gly Leu
 85 90 95
 Ile Met Ala Arg Lys Leu Ile His Leu Glu Ile Lys Pro Ala Ile Arg
 100 105 110

Asn	Gln	Ile	Ile	Arg	Glu	Leu	Gln	Val	Leu	His	Glu	Cys	Asn	Ser	Pro	115	120	125
Tyr	Ile	Val	Gly	Phe	Tyr	Gly	Ala	Phe	Tyr	Ser	Asp	Gly	Glu	Ile	Ser	130	135	140
Ile	Cys	Met	Glu	His	Met	Asp	Gly	Gly	Ser	Leu	Asp	Gln	Val	Leu	Lys	145	150	155
Glu	Ala	Lys	Arg	Ile	Pro	Glu	Glu	Ile	Leu	Gly	Lys	Val	Ser	Ile	Ala	165	170	175
Val	Leu	Arg	Gly	Leu	Ala	Tyr	Leu	Arg	Glu	Lys	His	Gln	Ile	Met	His	180	185	190
Arg	Asp	Val	Lys	Pro	Ser	Asn	Ile	Leu	Val	Asn	Ser	Arg	Gly	Glu	Ile	195	200	205
Lys	Leu	Cys	Asp	Phe	Gly	Val	Ser	Gly	Gln	Leu	Ile	Asp	Ser	Met	Ala	210	215	220
Asn	Ser	Phe	Val	Gly	Thr	Arg	Ser	Tyr	Met	Ala	Pro	Glu	Arg	Leu	Gln	225	230	235
Gly	Thr	His	Tyr	Ser	Val	Gln	Ser	Asp	Ile	Trp	Ser	Met	Gly	Leu	Ser	245	250	255
Leu	Val	Glu	Leu	Ala	Val	Gly	Arg	Tyr	Pro	Ile	Pro	Pro	Pro	Asp	Ala	260	265	270
Lys	Glu	Leu	Glu	Ala	Ile	Phe	Gly	Arg	Pro	Val	Val	Asp	Gly	Glu	Glu	275	280	285
Gly	Glu	Pro	His	Ser	Ile	Ser	Pro	Arg	Pro	Arg	Pro	Pro	Gly	Arg	Pro	290	295	300
Val	Ser	Gly	His	Gly	Met	Asp	Ser	Arg	Pro	Ala	Met	Ala	Ile	Phe	Glu	305	310	315
Leu	Leu	Asp	Tyr	Ile	Val	Asn	Glu	Pro	Pro	Pro	Lys	Leu	Pro	Asn	Gly	325	330	335
Val	Phe	Thr	Pro	Asp	Phe	Gln	Glu	Phe	Val	Asn	Lys	Cys	Leu	Ile	Lys	340	345	350
Asn	Pro	Ala	Glu	Arg	Ala	Asp	Leu	Lys	Met	Leu	Thr					355	360	

<210> 65

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR PRIMER

<400> 65
 cagagcaaag aagtttcttg ga 22

<210> 66
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR PROBE
 PRIMER

<400> 66
 tgaaacagca ctacttaagt ccaagtcga 29

<210> 67
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR PRIMER

<400> 67
 tctcatgagg acatcacatt tg 22

<210> 68
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR PRIMER

<400> 68
 agatggcatc ctctctgaag ,at 22

<210> 69
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR PROBE
 PRIMER

<400> 69
 cctgctttgc attctttgca ggct 24

<210> 70
 <211> 22

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: PCR PRIMER

 <400> 70
 aacgtccttg ctgtgtacaa gt 22

 <210> 71
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: PCR PRIMER

 <400> 71
 aaagtcagca ttgcggttct c 21

 <210> 72
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: PCR PROBE
 PRIMER

 <400> 72
 cttggcgtac ctccgagaga agcacc 26

 <210> 73
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: PCR PRIMER

 <400> 73
 gcttcacatt tcggtgcatg 20

 <210> 74
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: PCR PRIMER

 <400> 74
 gctggaggag ctggaactt 19

<210> 75
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR PROBE
PRIMER

<400> 75
aagcctttct cacccagaaa gccaaag

26

<210> 76
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR PRIMER

<400> 76
tttcgaagtc atcgtctttg a

21

<210> 77
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR PRIMER

<400> 77
catgagggct tccattacat ca

22

<210> 78
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR PROBE
PRIMER

<400> 78
agctgacca gaagacccag gacctc

26

<210> 79
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR PRIMER

<400> 79
 gcgtgttccc aatgctcagt 20

<210> 80
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR PRIMER

<400> 80
 ggaaagtcag cattgcggtt 20

<210> 81
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR PROBE
 PRIMER

<400> 81
 cttggcgtac ctccgagaga agcacc 26

<210> 82
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR PRIMER

<400> 82
 ttcacatttc ggtgcatgat c 21

<210> 83
 <211> 66
 <212> PRT
 <213> Homo sapiens

<400> 83
 Arg Lys Pro Met Leu Pro Ala Leu Thr Ile Asn Pro Thr Ile Ala Glu
 1 5 10 15
 Gly Pro Ser Pro Thr Ser Glu Gly Ala Ser Glu Ala Asn Leu Val Asp
 20 25 30
 Leu Gln Lys Lys Leu Glu Glu Leu Glu Leu Asp Glu Gln Gln Lys Arg

35 40 45
 Leu Glu Ala Phe Leu Thr Gln Lys Ala Lys Val Gly Glu Leu Lys Asp
 50 55 60
 Asp Asp
 65

<210> 84
 <211> 66
 <212> PRT
 <213> *Cricetulus griseus*

<400> 84
 Pro Lys Lys Lys Pro Thr Pro Ile Gln Leu Asn Pro Thr Pro Asp Gly
 1 5 10 15
 Ser Ala Val Asn Gly Thr Ser Ser Ala Glu Thr Asn Leu Glu Ala Leu
 20 25 30
 Gln Lys Lys Leu Glu Glu Leu Glu Leu Glu Glu Gln Gln Arg Asn Arg
 35 40 45
 Leu Glu Ala Phe Leu Thr Gln Lys Gln Lys Val Gly Glu Leu Lys Asp
 50 55 60
 Asp Asp
 65

<210> 85
 <211> 66
 <212> PRT
 <213> *Homo sapiens*

<400> 85
 Pro Lys Lys Lys Pro Thr Pro Ile Gln Leu Asn Pro Ala Pro Asp Gly
 1 5 10 15
 Ser Ala Val Asn Gly Thr Ser Ser Ala Glu Thr Asn Leu Glu Ala Leu
 20 25 30
 Gln Lys Lys Leu Glu Glu Leu Glu Leu Asp Glu Gln Gln Arg Lys Arg
 35 40 45
 Leu Glu Ala Phe Leu Thr Gln Lys Gln Lys Val Gly Glu Leu Lys Asp
 50 55 60
 Asp Asp
 65

<210> 86
 <211> 66
 <212> PRT
 <213> *Mus musculus*

<400> 86

Pro Lys Lys Lys Pro Thr Pro Ile Gln Leu Asn Pro Ala Pro Asp Gly
1 5 10 15

Ser Ala Val Asn Gly Thr Ser Ser Ala Glu Thr Asn Leu Glu Ala Leu
20 25 30

Gln Lys Lys Leu Glu Glu Leu Glu Leu Asp Glu Gln Gln Arg Lys Arg
35 40 45

Leu Glu Ala Phe Leu Thr Gln Lys Gln Lys Val Gly Glu Leu Lys Asp
50 55 60

Asp Asp
65

<210> 87

<211> 66

<212> PRT

<213> *Oryctolagus cuniculus*

<400> 87

Pro Lys Lys Lys Pro Thr Pro Ile Gln Leu Asn Pro Ala Pro Asp Gly
1 5 10 15

Ser Ala Val Asn Gly Thr Ser Ser Ala Glu Thr Asn Leu Glu Ala Leu
20 25 30

Gln Lys Lys Leu Glu Glu Leu Glu Leu Asp Glu Gln Gln Arg Lys Arg
35 40 45

Leu Glu Ala Phe Leu Thr Gln Lys Gln Lys Val Gly Glu Leu Lys Asp
50 55 60

Asp Asp
65

<210> 88

<211> 66

<212> PRT

<213> *Rattus norvegicus*

<400> 88

Pro Lys Lys Lys Pro Thr Pro Ile Gln Leu Asn Pro Ala Pro Asp Gly
1 5 10 15

Ser Ala Val Asn Gly Thr Ser Ser Ala Glu Thr Asn Leu Glu Ala Leu
20 25 30

Gln Lys Lys Leu Glu Glu Leu Glu Leu Asp Glu Gln Gln Arg Lys Arg
35 40 45

Leu Glu Ala Phe Leu Thr Gln Lys Gln Lys Val Gly Glu Leu Lys Asp
50 55 60

Asp Asp
65

<210> 89
<211> 66
<212> PRT
<213> *Xenopus laevis*

<400> 89
Pro Lys Lys Lys Pro Thr Pro Ile Gln Leu Asn Pro Asn Pro Glu Gly
1 5 10 15
Thr Ala Val Asn Gly Thr Pro Thr Ala Glu Thr Asn Leu Glu Ala Leu
20 25 30
Gln Lys Lys Leu Glu Glu Leu Glu Leu Asp Glu Gln Gln Arg Lys Arg
35 40 45
Leu Glu Ala Phe Leu Thr Gln Lys Gln Lys Val Gly Glu Leu Lys Asp
50 55 60

Asp Asp
65

<210> 90
<211> 66
<212> PRT
<213> *Cyprinus carpio*

<400> 90
Pro Lys Arg Arg Pro Val Pro Leu Ile Ile Ala Pro Thr Gly Glu Gly
1 5 10 15
Gln Ser Thr Asn Ile Asp Ala Ala Ser Glu Ala Asn Leu Glu Ala Leu
20 25 30
Gln Arg Lys Leu Gly Glu Leu Asp Leu Asp Glu Gln Gln Arg Lys Arg
35 40 45
Leu Glu Ala Phe Leu Thr Gln Lys Ala Gln Val Gly Glu Leu Lys Asp
50 55 60

Glu Asp
65

<210> 91
<211> 69
<212> PRT
<213> *Gallus gallus*

<400> 91
Met Pro Ala Lys Arg Lys Pro Val Leu Pro Ala Leu Thr Ile Thr Pro
1 5 10 15

Ser Pro Ala Glu Gly Pro Gly Pro Gly Gly Ser Ala Glu Ala Asn Leu
20 25 30

Val Asp Leu Gln Lys Lys Leu Glu Glu Leu Glu Leu Asp Glu Gln Gln
35 40 45

Lys Lys Arg Leu Glu Ala Phe Leu Thr Gln Lys Ala Lys Val Gly Glu
50 55 60

Leu Lys Asp Asp Asp
65

<210> 92
<211> 67
<212> PRT
<213> Homo sapiens

<400> 92
Arg Lys Pro Val Leu Pro Ala Leu Thr Ile Asn Pro Thr Ile Ala Glu
1 5 10 15

Gly Pro Ser Pro Thr Ser Glu Gly Ala Ser Glu Ala Asn Leu Val Asp
20 25 30

Leu Gln Lys Lys Leu Glu Glu Leu Glu Leu Asp Glu Gln Gln Lys Lys
35 40 45

Arg Leu Glu Ala Phe Leu Thr Gln Lys Ala Lys Val Gly Glu Leu Lys
50 55 60

Asp Asp Asp
65

<210> 93
<211> 67
<212> PRT
<213> Mus musculus

<400> 93
Arg Lys Pro Val Leu Pro Ala Leu Thr Ile Asn Pro Thr Ile Ala Glu
1 5 10 15

Gly Pro Ser Pro Thr Ser Glu Gly Ala Ser Glu Ala Asn Leu Val Asp
20 25 30

Leu Gln Lys Lys Leu Glu Glu Leu Asp Leu Asp Glu Gln Gln Arg Lys
35 40 45

Arg Leu Glu Ala Phe Leu Thr Gln Lys Ala Lys Val Gly Glu Leu Lys
50 55 60

Asp Asp Asp
65

<210> 94
 <211> 67
 <212> PRT
 <213> Rattus norvegicus

<400> 94
 Arg Lys Pro Val Leu Pro Ala Leu Thr Ile Asn Pro Thr Ile Ala Glu
 1 5 10 15
 Gly Pro Ser Pro Thr Ser Glu Gly Ala Ser Glu Ala His Leu Val Asp
 20 25 30
 Leu Gln Lys Lys Leu Glu Glu Leu Asp Leu Asp Glu Gln Gln Arg Lys
 35 40 45
 Arg Leu Glu Ala Phe Leu Thr Gln Lys Ala Lys Val Gly Glu Leu Lys
 50 55 60
 Asp Asp Asp
 65

<210> 95
 <211> 66
 <212> PRT
 <213> Homo sapiens

<400> 95
 Arg Lys Pro Met Leu Pro Ala Leu Thr Ile Asn Pro Thr Ile Ala Glu
 1 5 10 15
 Gly Pro Ser Pro Thr Ser Glu Gly Ala Ser Glu Ala Asn Leu Val Asp
 20 25 30
 Leu Gln Lys Lys Leu Glu Glu Leu Glu Leu Asp Glu Gln Gln Lys Arg
 35 40 45
 Leu Glu Ala Phe Leu Thr Gln Lys Ala Lys Val Gly Glu Leu Lys Asp
 50 55 60
 Asp Asp
 65

<210> 96
 <211> 66
 <212> PRT
 <213> Cricetulus griseus

<400> 96
 Pro Lys Lys Lys Pro Thr Pro Ile Gln Leu Asn Pro Thr Pro Asp Gly
 1 5 10 15
 Ser Ala Val Asn Gly Thr Ser Ser Ala Glu Thr Asn Leu Glu Ala Leu
 20 25 30

Gln Lys Lys Leu Glu Glu Leu Glu Leu Glu Glu Gln Gln Arg Asn Arg
 35 40 45

Leu Glu Ala Phe Leu Thr Gln Lys Gln Lys Val Gly Glu Leu Lys Asp
 50 55 60

Asp Asp
 65

<210> 97
 <211> 66
 <212> PRT
 <213> Homo sapiens

<400> 97
 Pro Lys Lys Lys Pro Thr Pro Ile Gln Leu Asn Pro Ala Pro Asp Gly
 1 5 10 15

Ser Ala Val Asn Gly Thr Ser Ser Ala Glu Thr Asn Leu Glu Ala Leu
 20 25 30

Gln Lys Lys Leu Glu Glu Leu Glu Leu Asp Glu Gln Gln Arg Lys Arg
 35 40 45

Leu Glu Ala Phe Leu Thr Gln Lys Gln Lys Val Gly Glu Leu Lys Asp
 50 55 60

Asp Asp
 65

<210> 98
 <211> 66
 <212> PRT
 <213> Mus musculus

<400> 98
 Pro Lys Lys Lys Pro Thr Pro Ile Gln Leu Asn Pro Ala Pro Asp Gly
 1 5 10 15

Ser Ala Val Asn Gly Thr Ser Ser Ala Glu Thr Asn Leu Glu Ala Leu
 20 25 30

Gln Lys Lys Leu Glu Glu Leu Glu Leu Asp Glu Gln Gln Arg Lys Arg
 35 40 45

Leu Glu Ala Phe Leu Thr Gln Lys Gln Lys Val Gly Glu Leu Lys Asp
 50 55 60

Asp Asp
 65

<210> 99
 <211> 66
 <212> PRT

<213> *Oryctolagus cuniculus*

<400> 99

Pro Lys Lys Lys Pro Thr Pro Ile Gln Leu Asn Pro Ala Pro Asp Gly
1 5 10 15
Ser Ala Val Asn Gly Thr Ser Ser Ala Glu Thr Asn Leu Glu Ala Leu
20 25 30
Gln Lys Lys Leu Glu Glu Leu Glu Leu Asp Glu Gln Gln Arg Lys Arg
35 40 45
Leu Glu Ala Phe Leu Thr Gln Lys Gln Lys Val Gly Glu Leu Lys Asp
50 55 60
Asp Asp
65

<210> 100

<211> 66

<212> PRT

<213> *Rattus norvegicus*

<400> 100

Pro Lys Lys Lys Pro Thr Pro Ile Gln Leu Asn Pro Ala Pro Asp Gly
1 5 10 15
Ser Ala Val Asn Gly Thr Ser Ser Ala Glu Thr Asn Leu Glu Ala Leu
20 25 30
Gln Lys Lys Leu Glu Glu Leu Glu Leu Asp Glu Gln Gln Arg Lys Arg
35 40 45
Leu Glu Ala Phe Leu Thr Gln Lys Gln Lys Val Gly Glu Leu Lys Asp
50 55 60
Asp Asp
65

<210> 101

<211> 66

<212> PRT

<213> *Xenopus laevis*

<400> 101

Pro Lys Lys Lys Pro Thr Pro Ile Gln Leu Asn Pro Asn Pro Glu Gly
1 5 10 15
Thr Ala Val Asn Gly Thr Pro Thr Ala Glu Thr Asn Leu Glu Ala Leu
20 25 30
Gln Lys Lys Leu Glu Glu Leu Glu Leu Asp Glu Gln Gln Arg Lys Arg
35 40 45
Leu Glu Ala Phe Leu Thr Gln Lys Gln Lys Val Gly Glu Leu Lys Asp

50 55 60

Asp Asp
65

<210> 102
<211> 66
<212> PRT
<213> *Cyprinus carpio*

<400> 102
Pro Lys Arg Arg Pro Val Pro Leu Ile Ile Ala Pro Thr Gly Glu Gly
1 5 10 15
Gln Ser Thr Asn Ile Asp Ala Ala Ser Glu Ala Asn Leu Glu Ala Leu
 20 25 30
Gln Arg Lys Leu Gly Glu Leu Asp Leu Asp Glu Gln Gln Arg Lys Arg
 35 40 45
Leu Glu Ala Phe Leu Thr Gln Lys Ala Gln Val Gly Glu Leu Lys Asp
50 55 60
Glu Asp
65

<210> 103
<211> 67
<212> PRT
<213> *Gallus gallus*

<400> 103
Ala Lys Arg Lys Pro Val Leu Pro Ala Leu Thr Ile Thr Pro Ser Pro
1 5 10 15
Ala Glu Gly Pro Gly Pro Gly Gly Ser Ala Glu Ala Asn Leu Val Asp
20 25 30
Leu Gln Lys Lys Leu Glu Glu Leu Glu Leu Asp Glu Gln Gln Lys Lys
35 40 45
Arg Leu Glu Ala Phe Leu Thr Gln Lys Ala Lys Val Gly Glu Leu Lys
50 55 60
Asp Asp Asp
65

<210> 104
<211> 67
<212> PRT
<213> *Homo sapiens*

<400> 104
Arg Lys Pro Val Leu Pro Ala Leu Thr Ile Asn Pro Thr Ile Ala Glu

1 5 10 15
 Gly Pro Ser Pro Thr Ser Glu Gly Ala Ser Glu Ala Asn Leu Val Asp
 20 25 30
 Leu Gln Lys Lys Leu Glu Glu Leu Glu Leu Asp Glu Gln Gln Lys Lys
 35 40 45
 Arg Leu Glu Ala Phe Leu Thr Gln Lys Ala Lys Val Gly Glu Leu Lys
 50 55 60
 Asp Asp Asp
 65

<210> 105
 <211> 67
 <212> PRT
 <213> Mus musculus

<400> 105
 Arg Lys Pro Val Leu Pro Ala Leu Thr Ile Asn Pro Thr Ile Ala Glu
 1 5 10 15
 Gly Pro Ser Pro Thr Ser Glu Gly Ala Ser Glu Ala Asn Leu Val Asp
 20 25 30
 Leu Gln Lys Lys Leu Glu Glu Leu Asp Leu Asp Glu Gln Gln Arg Lys
 35 40 45
 Arg Leu Glu Ala Phe Leu Thr Gln Lys Ala Lys Val Gly Glu Leu Lys
 50 55 60
 Asp Asp Asp
 65

<210> 106
 <211> 67
 <212> PRT
 <213> Rattus norvegicus

<400> 106
 Arg Lys Pro Val Leu Pro Ala Leu Thr Ile Asn Pro Thr Ile Ala Glu
 1 5 10 15
 Gly Pro Ser Pro Thr Ser Glu Gly Ala Ser Glu Ala His Leu Val Asp
 20 25 30
 Leu Gln Lys Lys Leu Glu Glu Leu Asp Leu Asp Glu Gln Gln Arg Lys
 35 40 45
 Arg Leu Glu Ala Phe Leu Thr Gln Lys Ala Lys Val Gly Glu Leu Lys
 50 55 60
 Asp Asp Asp
 65

<210> 107
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: PCR PRIMER

 <400> 107
 ggatcccttc taaagccgag cttctcacca agg 33

 <210> 108
 <211> 37
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: PCR PRIMER

 <400> 108
 ctcgagtttt ccaatagggt taacaatctt tcccagg 37

 <210> 109
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: SEQUENCING
 PRIMER

 <400> 109
 tacatcatcc acgagctgac c 21

 <210> 110
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: SEQUENCING
 PRIMER

 <400> 110
 ggtcagctcg tggatgatc 19

 <210> 111
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: SEQUENCING
 PRIMER

<400> 111
 agttcagtca aggtgccc 18

<210> 112
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: SEQUENCING
 PRIMER

<400> 112
 gggcaccttg actgaactg 19

<210> 113
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: SEQUENCING
 PRIMER

<400> 113
 catggtgatc tcaccaagat cg 22

<210> 114
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: SEQUENCING
 PRIMER

<400> 114
 cgatcttggt gagatcacca tg 22

<210> 115
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR PRIMER

<400> 115
 ctcgtcctcg agggtaagcc tatccctaac 30

<210> 116
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: PCR PRIMER

 <400> 116
 ctcgtcgggc ccctgatcag cgggtttaa c 31

 <210> 117
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: PCR PRIMER

 <400> 117
 ggatccaaag aagtttcttg gagagaattc atg 33

 <210> 118
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: PCR PRIMER

 <400> 118
 ctcgaggttg ccgataggtt ctaccatc 28